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OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:45 ; Search time 12.9581 Seconds
(without alignments)
1524.850 Million cell updates/sec

Title: US-09-488-265B-29

Perfect score: 2462

Sequence: 1 MGFFVLLSLATLFGSTSGT.....DFVEGLSFARSGGNWAECA 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2408	97.8	467	4	US-09-273-871A-9
2	2282	92.7	441	3	US-09-121-425-1
3	2282	92.7	441	4	US-09-634-493A-1
4	2270	92.2	467	3	US-09-121-425-2
5	2270	92.2	467	4	US-09-634-493A-2
6	1879	76.3	467	1	US-07-923-724-8
7	1879	76.3	467	2	US-08-609-426A-8
8	1879	76.3	467	2	US-08-374-652C-2
9	1875	76.2	467	1	US-08-151-574-32
10	1875	76.2	467	1	US-08-146-424-20
11	1875	76.2	467	1	US-08-693-709-2
12	1875	76.2	467	2	US-08-419-448-32
13	1875	76.2	467	2	US-08-810-825-3
14	1875	76.2	467	3	US-09-163-642-3
15	1875	76.2	467	4	US-09-233-510-32
16	1875	76.2	467	4	US-09-636-499-5
17	1867	75.8	465	3	US-08-868-435-33
18	1867	75.8	465	4	US-08-744-211-33
19	1867	75.8	465	4	US-09-044-718-78
20	1867	75.8	465	4	US-09-636-499-6
21	1867	75.8	465	4	US-09-273-871A-8
22	1863	75.7	467	4	US-09-273-871A-11
23	1860	75.5	467	3	US-09-155-855-3
24	1860	75.5	467	4	US-09-543-744-3
25	1860	75.5	467	4	US-09-929-060-3
26	1859	75.5	465	4	US-09-044-718-80
27	1858	75.5	465	4	US-09-044-718-79

28	1857	75.4	439	4	US-09-044-718-3	Sequence 3, Appli
29	1857	75.4	449	4	US-09-044-718-12	Sequence 12, Appl
30	1855	75.3	465	4	US-09-044-718-81	Sequence 81, Appl
31	1851	75.2	462	4	US-09-636-499-12	Sequence 12, Appl
32	1845	74.9	469	4	US-09-044-718-82	Sequence 82, Appl
33	1839	74.7	466	3	US-08-868-435-35	Sequence 35, Appl
34	1839	74.7	466	4	US-08-744-231-35	Sequence 35, Appl
35	1835	74.6	463	3	US-08-868-435-29	Sequence 29, Appl
36	1835	74.6	463	4	US-08-744-231-29	Sequence 29, Appl
37	1835	74.6	463	4	US-09-273-871A-10	Sequence 10, Appl
38	1833	74.5	444	4	US-09-044-718-1	Sequence 1, Appli
39	1820	73.9	447	4	US-09-044-718-6	Sequence 6, Appli
40	1818	73.8	443	3	US-09-155-855-1	Sequence 1, Appli
41	1818	73.8	443	4	US-09-543-744-1	Sequence 1, Appli
42	1818	73.8	443	4	US-09-929-060-1	Sequence 1, Appli
43	1813	73.6	443	3	US-09-155-855-2	Sequence 2, Appli
44	1813	73.6	443	4	US-09-543-744-2	Sequence 2, Appli
45	1813	73.6	443	4	US-09-929-060-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-273-871A-9
; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273.871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Query Match 97.8%; Score 2408; DB 4; Length 467;

Best Local Similarity 97.9%; Pred. No. 1.9e-243;

Matches 457; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy	1	MGFFVLLSLATLFGSTSGTALGPRGNHSCDTVDGGYQCFPEISHLWGTYSFYFSLADE 60		
Db	1	MGFFVLLSLATLFGSTSGTALGPRGNHSCDTVDGGYQCFPEISHLWGTYSFYFSLADE 60		
Qy	61	SATSPDVPDDCRVTFQVLSRHGARYPTSSAKAYSALIEAOKNATAPKGYAFUKTYN 120		
Db	61	SATSPDVPDDCRVTFQVLSRHGARYPTSSAKAYSALIEAOKNATAPKGYAFUKTYN 120		
Qy	121	YTLGADDLTPFGENOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIAENKFIQFQSA 180		
Db	121	YTLGADDLTPFGENOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIAENKFIQFQSA 180		
Qy	181	KLADPGSQPHASPVINVIPEGSGYNNLTLDHGTCTAFDESELGDDVEANFTALFAPAIR 240		
Db	181	KLADPGSQPHASPVINVIPEGSGYNNLTLDHGTCTAFDESELGDDVEANFTALFAPAIR 240		

Db 181 KLADPGSOPHOASPVINDVTPEBSGYNNTLDHCTCTAFEDSHLGGDDVEANFTALFAPAIR 240
QY 241 ARLEADLPVGLTDEVDVYLMDMCPDFTVARTSDATELSPFCALFTHDEWIOYDYLQSLG 300
Db 241 ARLEADLPVGLTDEVDVYLMDMCPETVARTSDATELSPFCALFTHDEWIOYDYLQSLG 300
QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVDHSTNHTLDSNPATFPLNATLYAFDS 360
Db 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVDHSTNHTLDSNPATFPLNATLYAFDS 360
QY 361 HDNWTMISIFALGLYNGTKPLSTTSVESIETDGYASWTVPFAARAYVEMMOQAEKEP 420
Db 361 HDNWTMISIFALGLYNGTKPLSTTSVESIETDGYASWTVPFAARAYVEMMOQAEKEP 420
QY 421 LVRVLVNDVRVPLHGCACVADKLGRCKRDFVEGLSFARSGGNWAECEFA 467
Db 421 LVRVLVNDVRVPLHGCACVADKLGRCKRDFVEGLSFARSGGNWAECEFA 467

RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
US-09-121-425-1

Query Match 92.7%; Score 2282; DB 3; Length 441;
Best Local Similarity 97.7%; Pred. No. 2.8e-230;
Matches 431; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 27 NNSHCDTVGGYQCFFPEISHLWGTSPYFSLADESALSPDVPDCCRVTFFVQVLSRHGARY 86
Db 1 NNSHCDTVGGYQCFFPEISHLWGTSPYFSLADESALSPDVPDCCRVTFFVQVLSRHGARY 60
QY 87 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLGGADDLTPFGENQMVNSGKIFYRR 146
Db 61 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLGGADDLTPFGENQMVNSGKIFYRR 120
QY 147 YKALARKIVPFIIRASGSDRVIASAEKFIIEGFSQAKLADPGSQPHOASPVINVIIPESGY 206
Db 121 YKALARKIVPFIIRASGSDRVIASAEKFIIEGFSQAKLADPGSQPHOASPVINVIIPESGY 180
QY 207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVGLTDEVDVYLMDMCP 266
Db 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVGLTDEVDVYLMDMCP 240
QY 267 DTVAKTSDATELSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 326
Db 241 EIVARTSDATELSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 300
QY 327 LTHSPVDHSTNHTLDSNPATFPLNATLYADFSHDNWTMISIFFALGLYNGTKPLSTTSV 386
Db 301 LTHSPVDHSTNHTLDSNPATFPLNATLYADFSHDNWTMISIFFALGLYNGTKPLSTTSV 360
QY 387 ESIEETDGYASWTVPFAARAYVEMMOQAEKEPLVRVLVNDVRVPLHGCACVADKLGRCKR 446
Db 361 ESIEETDGYASWTVPFAARAYVEMMOQAEKEPLVRVLVNDVRVPLHGCACVADKLGRCKR 420

QY 447 DDFVEGLSFARSGGNWAECEFA 467
Db 421 DDFVEGLSFARSGGNWAECEFA 441

RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634.493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121.425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
US-09-634-493A-1

Query Match 92.7%; Score 2282; DB 4; Length 441;
Best Local Similarity 97.7%; Pred. No. 2.8e-230;
Matches 431; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 27 NNSHCDTVGGYQCFFPEISHLWGTSPYFSLADESALSPDVPDCCRVTFFVQVLSRHGARY 86
Db 1 NNSHCDTVGGYQCFFPEISHLWGTSPYFSLADESALSPDVPDCCRVTFFVQVLSRHGARY 60
QY 87 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLGGADDLTPFGENQMVNSGKIFYRR 146
Db 61 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLGGADDLTPFGENQMVNSGKIFYRR 120
QY 147 YKALARKIVPFIIRASGSDRVIASAEKFIIEGFSQAKLADPGSQPHOASPVINVIIPESGY 206
Db 121 YKALARKIVPFIIRASGSDRVIASAEKFIIEGFSQAKLADPGSQPHOASPVINVIIPESGY 180
QY 207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVGLTDEVDVYLMDMCP 266
Db 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVGLTDEVDVYLMDMCP 240
QY 267 DTVAKTSDATELSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 326
Db 241 EIVARTSDATELSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 300
QY 327 LTHSPVDHSTNHTLDSNPATFPLNATLYADFSHDNWTMISIFFALGLYNGTKPLSTTSV 386
Db 301 LTHSPVDHSTNHTLDSNPATFPLNATLYADFSHDNWTMISIFFALGLYNGTKPLSTTSV 360
QY 387 ESIEETDGYASWTVPFAARAYVEMMOQAEKEPLVRVLVNDVRVPLHGCACVADKLGRCKR 446
Db 361 ESIEETDGYASWTVPFAARAYVEMMOQAEKEPLVRVLVNDVRVPLHGCACVADKLGRCKR 420

RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:

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; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-09-121-425-2

Query Match          92.2%; Score 2270; DB 3; Length 467;
Best Local Similarity 89.7%; Pred. No. 5.5e-229;
Matches 437; Conservative 3; Mismatches 7; Indels 40; Gaps 2;

QY 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTDDGGYQCFFPEISHLWGTSPYFSLADE 60
DB 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTDDGGYQCFFPEISHLWGTSPYFSLADE 60
QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
DB 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 180
DB 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 180
QY 101 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 160
DB 101 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 160
QY 181 KLADPGSQPHQASPVIN-----VIIPEGSGYNTLDHGCTAFED 220
DB 181 KLADPGSQPHQASPVIN-----VIIPEGSGYNTLDHGCTAFED 220
QY 161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGYAFLKVIIPFEGSGYNTLDHGCTAFED 220
DB 161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGYAFLKVIIPFEGSGYNTLDHGCTAFED 220
QY 221 SELGDDVEANFTALFAPAIRLEADLPVTLTDEDVYVLMDCPFDVARTSDATELSP 280
DB 221 SELGDDVEANFTALFAPAIRLEADLPVTLTDEDVYVLMDCPFDVARTSDATELSP 280
QY 281 FCALFTHDEWQYDYLSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
DB 281 FCALFTHDEWQYDYLSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
QY 341 TLDSNPATPLNATLYADFSHDNIMISIFFALGLYNGIKPLSTTSVESIEETDGYASWT 400
DB 341 TLDSNPATPLNATLYADFSHDNIMISIFFALGLYNGIKPLSTTSVESIEETDGYASWT 400
QY 401 VPFAARAYVEMMQCAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKRDDEFVGLSFARSGG 460
DB 401 VPFAARAYVEMMQCAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKRDDEFVGLSFARSGG 460
QY 461 NWAECFA 467
DB 461 NWAECFA 467

RESULT 6
US-07-923-724-8
; Sequence 8, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington

; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-09-121-425-2

Query Match          92.2%; Score 2270; DB 3; Length 467;
Best Local Similarity 89.7%; Pred. No. 5.5e-229;
Matches 437; Conservative 3; Mismatches 7; Indels 40; Gaps 2;

QY 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTDDGGYQCFFPEISHLWGTSPYFSLADE 60
DB 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTDDGGYQCFFPEISHLWGTSPYFSLADE 60
QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
DB 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 180
DB 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 180
QY 101 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 160
DB 101 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 160
QY 181 KLADPGSQPHQASPVIN-----VIIPEGSGYNTLDHGCTAFED 220
DB 181 KLADPGSQPHQASPVIN-----VIIPEGSGYNTLDHGCTAFED 220
QY 161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGYAFLKVIIPFEGSGYNTLDHGCTAFED 220
DB 161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGYAFLKVIIPFEGSGYNTLDHGCTAFED 220
QY 221 SELGDDVEANFTALFAPAIRLEADLPVTLTDEDVYVLMDCPFDVARTSDATELSP 280
DB 221 SELGDDVEANFTALFAPAIRLEADLPVTLTDEDVYVLMDCPFDVARTSDATELSP 280
QY 281 FCALFTHDEWQYDYLSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
DB 281 FCALFTHDEWQYDYLSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
QY 341 TLDSNPATPLNATLYADFSHDNIMISIFFALGLYNGIKPLSTTSVESIEETDGYASWT 400
DB 341 TLDSNPATPLNATLYADFSHDNIMISIFFALGLYNGIKPLSTTSVESIEETDGYASWT 400
QY 401 VPFAARAYVEMMQCAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKRDDEFVGLSFARSGG 460
DB 401 VPFAARAYVEMMQCAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKRDDEFVGLSFARSGG 460
QY 461 NWAECFA 467
DB 461 NWAECFA 467

RESULT 5
US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634,493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121.425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
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STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0240004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-724-8

Query Match 76.3%, Score 1879; DB 1: Length 467;
Best Local Similarity 75.6%, Pred. No. 5.1e-188;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVSFVLLSVATLFGSTGSGTALPGRNSHSCDVTVDGGYQCFPEISHLWGTYSYFSLADE 60
DB 1 MGVSFVLLSVATLFGSTGSGTALPGRNSHSCDVTVDGGYQCFPEISHLWGTYSYFSLADE 60

QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEIAOKNATAFKGYAFKLTYN 120
DB 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEIAOKNATAFKGYAFKLTYN 120

QY 121 YTLGADDLTPFGENOMVNSGKIFVRYRKALARKIVPFIRASGSDRVIASAEKFIQFQSA 180
DB 121 YTLGADDLTPFGENOMVNSGKIFVRYRKALARKIVPFIRASGSDRVIASAEKFIQFQSA 180

QY 181 KLADPGSQHOASPVINVIPEGSGYNTLDHGTCTAFEDSELGDDVEANFTALEAPAIR 240
DB 181 KLADPGSQHOASPVINVIPEGSGYNTLDHGTCTAFEDSELGDDVEANFTALEAPAIR 240

QY 241 ARLEADLPVLTDEDVYVLMDCPFTVARTSDATFSLFPCALFTHDEWIQDYLOSIG 300
DB 241 ARLEADLPVLTDEDVYVLMDCPFTVARTSDATFSLFPCALFTHDEWIQDYLOSIG 300

QY 301 KYCYGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADES 360
DB 301 KYCYGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADES 360

QY 361 HDNMTSIFPALGYNKTPSTSVSEIETDGYASNTVPFAARAYVEMQOAEKEP 420
DB 361 HDNMTSIFPALGYNKTPSTSVSEIETDGYASNTVPFAARAYVEMQOAEKEP 420

QY 421 LVRVLNDRVPLHGCQVADKGRCKRDDFVEGLSFARSGGNWAECA 467
DB 421 LVRVLNDRVPLHGCQVADKGRCKRDDFVEGLSFARSGGNWAECA 467

RESULT 7
US-09-609-426A-8
Sequence 8, Application US/08609426A
Patent No. 5830733
GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerström, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant E.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 1050.0080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-609-426A-8

Query Match 76.3%, Score 1879; DB 2: Length 467;
Best Local Similarity 75.6%, Pred. No. 5.1e-188;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVSFVLLSVATLFGSTGSGTALPGRNSHSCDVTVDGGYQCFPEISHLWGTYSYFSLADE 60
DB 1 MGVSFVLLSVATLFGSTGSGTALPGRNSHSCDVTVDGGYQCFPEISHLWGTYSYFSLADE 60

QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEIAOKNATAFKGYAFKLTYN 120
DB 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEIAOKNATAFKGYAFKLTYN 120

QY 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALAKKIVPFIASGSDRVIASAKKFEIGFQSA 180
D 121 YSLGADDLTPFGENQMVNSGKIFRYRYKALAKKIVPFIASGSDRVIASAKKFEIGFQSA 180
QY 181 KLADPGSOPHOASPVINIIPEGSGYNNLTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
D 181 KLKOPRQPGGSSPKIDVISEASSNNLTDPGCTVFEDSELADTVANFTATFAPAIR 240
QY 241 ARLEADLFGVTLTDEVDVYLMDCPFDTVARTSDATLSLPCALFTHDEWIYDYLQSLG 300
D 241 ORLENDLSGVTLTDEVTYLMDCSFDTISTVDTKLSPCDLFTHDEWIYDYLQSLK 300
QY 301 KYYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHLSDSNPATFPLNATLYADFS 360
D 301 KYYGAGNPLGPTQGVGYANELIARLTHSPVHDOTSSNHLSDSNPATFPLNATLYADFS 360
QY 361 HONTMISIFFALGLYNGTKPLSTTSVESIEETDGYASASWTVPFAARAYVENMOCQAEKP 420
D 361 HDNGIISILFALGLYNGTKPLSTTVENITQDGFSSAWTVPFASRLYVENMOCQAEQP 420
QY 421 LVRVLNDRVPLHGCANDKLGCRKRDDEFVEGLSFARSGGNNAECFA 467
D 421 LVRVLNDRVPLHGCIPDALGRCTRDSEFVRLSPARSGGDAECFA 467

RESULT 8

US-08-374-652C-2
Sequence 2, Application US/08374652C
Patent No. 5834286
GENERAL INFORMATION:
APPLICANT: NEVALAINEN, HELENA K.M.
APPLICANT: PALOHEIMO, MARJA T.
APPLICANT: FAGERSTROM, RICHARD B.
APPLICANT: MIETTINEN-OINONEN, ARJA S.
APPLICANT: TURUNEN, MARJA K.
APPLICANT: RAMBOSEK, JOHN A.
APPLICANT: PIDDINGTON, CHRISTOPHER S.
APPLICANT: HOUSION, CHRISTINE S.
APPLICANT: CANIRELL, MICHAEL A.
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 1050.071001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-374-652C-2
Query Match 76.3%, Score 1879; DB 2: Length 467;
Best Local Similarity 75.6%, Pred. No. 5, le-188;
Matches 333; Conservative 41; Mismatches 73; Indels 0; Gaps 0;
QY 1 MGVEVVLSTLFGSTSGTALGPRGNSHSDTVGVGYOCFPEISHLMGTSPYPSLADE 60
D 1 MGVSAYVLLPLYLAGVTSGLVAPASRNQSTCDTVDQGYOCFSETSHLMGOYAPFFSLANE 60
QY 61 SATSPDVPDCRVTFYQVLSRHGARYPTSSAKYASALIEAQKNAIAFKGYAFKTYN 120
D 61 SATSPDVPACRVTFYQVLSRHGARYPTESKGYKYSALIEEQVNTTFDGYAFKTYN 120
QY 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALAKKIVPFIASGSDRVIASAKKFEIGFQSA 180
D 121 YSLGADDLTPFGENQMVNSGKIFRYRYKALAKKIVPFIASGSDRVIASAKKFEIGFQST 180
QY 181 KLADPGSOPHOASPVINIIPEGSGYNNLTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
D 181 KLKOPRQPGGSSPKIDVISEASSNNLTDPGCTVFEDSELADTVANFTATFAPAIR 240
QY 241 ARLEADLFGVTLTDEVDVYLMDCPFDTVARTSDATLSLPCALFTHDEWIYDYLQSLG 300
D 241 ORLENDLSGVTLTDEVTYLMDCSFDTISTVDTKLSPCDLFTHDEWIYDYLQSLK 300
QY 301 KYYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHLSDSNPATFPLNATLYADFS 360
D 301 KYYGAGNPLGPTQGVGYANELIARLTHSPVHDOTSSNHLSDSNPATFPLNATLYADFS 360
QY 361 HONTMISIFFALGLYNGTKPLSTTSVESIEETDGYASASWTVPFAARAYVENMOCQAEKP 420
D 361 HDNGIISILFALGLYNGTKPLSTTVENITQDGFSSAWTVPFASRLYVENMOCQAEQP 420
QY 421 LVRVLNDRVPLHGCANDKLGCRKRDDEFVEGLSFARSGGNNAECFA 467
D 421 LVRVLNDRVPLHGCIPDALGRCTRDSEFVRLSPARSGGDAECFA 467

RESULT 9

US-08-151-574-32
Sequence 32, Application US/08151574
Patent No. 5436156
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Seltin
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

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; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 25,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-151-574-32

Query Match 75.28; Score 1875; DB 1; Length 467;
Best Local Similarity 75.68; Pred. No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVEVLLSIATLFGSTSGTALGPRGNHSCDVTGGYQCFFPEISHLMGTSPYFSLADP 60
DB 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLMGQYAPFFSLANE 60
QY 61 SAISPDPDCCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLLKTYN 120
DB 61 SVISPEVAGCRVTFVQVLSRHGARYPTDSKGGKYSALIEIQKNATTFDGKYAFLLKTYN 120
QY 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPPIRASGSDRVIASAEKIEGFQSA 180
DB 121 YSLGADDLTPFGEQELVNSGKIFQRYESLTRNIVPPIRSGSSRVIASGKKFIEGFQST 180
QY 181 KLADPGSQPHQASPVINVIIEPGSGYNNTLDHGCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLKDPRAQPGQSSPKIDVISEASSNNILDPGCTVFEDSELADTVEANFTATVPFSIR 240
QY 241 ARLEADLPGLVTLTDEDVYVLMDCPFDVTARTSDATELSDFCALFTHDEWIQYDYLSLG 300
DB 241 QRLNDLSGVTLTDEVTYVLMDCSFDITSTVDTKLSPCDLFTHDEWINDYDYLSLK 300
QY 301 KYYGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 KYYGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360
QY 361 HDNTMISIFFALGLYNGTKPLSTTSVESIETDGYASWTVPFAARAYVEMQCAKEP 420
DB 361 HDNGIISILFALGLYNGTKPLSTTIVENITQDGFSSANTVPFASRLYVEMQCAEQEP 420
QY 421 LVRVLNDRVPLHGCPCVDALGRCTRDSFVRGLSFARSGGDAECFA 467
DB 421 LVRVLNDRVPLHGCPCVDALGRCTRDSFVRGLSFARSGGDAECFA 467

RESULT 10
US-08-146-424-20
; Sequence 20, Application US/08:46424
; Patent No. 5593963
; GENERAL INFORMATION:
; APPLICANT: VAN OOIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

```

```

;
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,424
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: 44615-20011.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-146-424-20

Query Match 76.28; Score 1875; DB 1; Length 467;
Best Local Similarity 75.68; Pred. No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVEVLLSIATLFGSTSGTALGPRGNHSCDVTGGYQCFFPEISHLMGTSPYFSLADE 60
DB 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLMGQYAPFFSLANE 60
QY 61 SAISPDPDCCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLLKTYN 120
DB 61 SVISPEVAGCRVTFVQVLSRHGARYPTDSKGGKYSALIEIQKNATTFDGKYAFLLKTYN 120
QY 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPPIRASGSDRVIASAEKIEGFQSA 180
DB 121 YSLGADDLTPFGEQELVNSGKIFQRYESLTRNIVPPIRSGSSRVIASGKKFIEGFQST 180
QY 181 KLADPGSQPHQASPVINVIIEPGSGYNNTLDHGCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLKDPRAQPGQSSPKIDVISEASSNNILDPGCTVFEDSELADTVEANFTATVPFSIR 240
QY 241 ARLEADLPGLVTLTDEDVYVLMDCPFDVTARTSDATELSDFCALFTHDEWIQYDYLSLG 300
DB 241 QRLNDLSGVTLTDEVTYVLMDCSFDITSTVDTKLSPCDLFTHDEWINDYDYLSLK 300
QY 301 KYYGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 KYYGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360
QY 361 HDNTMISIFFALGLYNGTKPLSTTSVESIETDGYASWTVPFAARAYVEMQCAKEP 420
DB 361 HDNGIISILFALGLYNGTKPLSTTIVENITQDGFSSANTVPFASRLYVEMQCAEQEP 420
QY 421 LVRVLNDRVPLHGCPCVDALGRCTRDSFVRGLSFARSGGDAECFA 467
DB 421 LVRVLNDRVPLHGCPCVDALGRCTRDSFVRGLSFARSGGDAECFA 467

RESULT 11
US-08-693-709-2
; Sequence 2, Application US/08693709
; Patent No. 5770413
; GENERAL INFORMATION:

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QY	301	KYYGAGNPLGPAQGVGFANELIARLTHSPVQCHTSTNHTLDSNPATPLNATLYADFS	360
DB	301	KYYGAGNPLGPTQGVGVANELIARLTHSPVHDITSSNHTLDSNPATPLNATLYADFS	360
QY	361	HDNTMISIFALGLYNGTGPLSTTSVESIEETDGTGSASWTVPFAARAYVEMHQAQEP	420
DB	361	HDNGIISILFALGLYNGTGPLSTTTVENITQDGFSAWTFPASRLYVEMHQAQEP	420
QY	421	LVRVLYNDRVVPLRGCAVDKLGRCRDEVEGLSFARSGGMAECFA	467
DB	421	LVRVLYNDRVVPLRGCPVDALGRCTRDSFVRLGSLFARSGGDNAECFA	467
<p>RESULT 12</p> <p>US-08-419-448-32</p> <p>Sequence 32, Application US/08419448</p> <p>Patent No. 5863533</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Robert F.M. Van Gortcom</p> <p>APPLICANT: Willem Van Hartingsveldt</p> <p>APPLICANT: Petrus A. Van Paridon</p> <p>APPLICANT: Annemarie E. Veenstra</p> <p>APPLICANT: Rudolf G.M. Luttin</p> <p>APPLICANT: Gerardus Seltin</p> <p>TITLE OF INVENTION: Cloning and Expression of Microbial</p> <p>TITLE OF INVENTION: Phytase</p> <p>NUMBER OF SEQUENCES: 52</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Morrison & Foerster</p> <p>STREET: 2000 Pennsylvania Ave. N.W., Suite 5500</p> <p>CITY: Washington</p> <p>STATE: D.C.</p> <p>COUNTRY: USA</p> <p>ZIP: 20006-1888</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: PatentIn Release #1.0, Version #1.25</p> <p>SOFTWARE:</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: JS/08/419,448</p> <p>FILING DATE: 10-APR-1995</p> <p>CLASSIFICATION: 435</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Murashige, Kate H.</p> <p>REGISTRATION NUMBER: 29,959</p> <p>REFERENCE/DOCKET NUMBER: 24615-20026.10</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 202-887-1500</p> <p>INFORMATION FOR SEQ ID NO: 32:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 467 amino acids</p> <p>TYPE: amino acid</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: protein</p> <p>US-08-419-448-32</p>			
<p>Query Match 76.2%; Score 1875; DB 1; Length 467;</p> <p>Best Local Similarity 75.6%; Pred. No. 1.3e-187;</p> <p>Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;</p>			
QY	1	MGVAVLLSLATLFGSTGTALGPRNSHSCDTPDGGYQCPEISHLWGTSPYFSLADE	60
DB	1	MGVAVLLPLLYLLSGVTSLAVPASRNQSCDTPDQGYQCFSETSHLWGTAPFFSLANE	60
QY	61	SAISPDVDDCRVTFVQVLSRHARGARYPTSSASKAYSALIEAIQKNATAFKGYAFKLTYN	120
DB	61	SVISPEVPACGRVTFQAQLSRHARGARYPTDSKGGKYSALIEETQNNATFDGKYAFKLTYN	120
QY	121	YTLGADDLTPFGENQWNSGKIFRYRYKALARKIVPFIKASGSDRVIAAEKFIQFQSA	180
DB	121	YSLGADLLTPFGEQLVNSGKIFRYRYKALARKIVPFIKASGSDRVIAAEKFIQFQSA	180
QY	181	KLADPGSQPQASPVINVIPEGSGVNNITDGTCTAFEDSLGDDVEANFTALFAPAIR	240
DB	181	KUKDPRAQPGSQPKIDVIVSEASSNNTLDPTCTVFEDSLATVEANFTALFAPAIR	240
QY	241	ARLEADLPQVTLTDEVDVYLMDCPFDVAVTSNTELSPPFCALFTHDEWIDYQLSLG	300
DB	241	QRENDLSQVTLTDEVDVYLMDCPFDVAVTSNTELSPPFCALFTHDEWIDYQLSLG	300

Db 121 YSLGADDLTPFGEQELVNSGIRFYQRYESLNRNIVPFIIRSSGSRVSIASKKFIEGFQST 180
QY 181 KLADPGSQPHQASPVINVIIPESGYNNLTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db 181 KLKDPRAQPGQSPKIDVVISSEASSNLTDPGTCTVFEDSELADTVEANFTAFVPSIR 240
QY 241 ARLEADLPQVTLTDEDVYVLMDCPFDTVARTSDATELSPFCALFTHDEWIQDYVLQSLG 300
Db 241 QRLNDLSGVTLTDEVYVLMDCSFDTISTVDTKLSPPFCDLFTHDEWINDYVLQSLK 300
QY 301 KYGYGAGNPLGPAQGVGFANELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db 301 KYGYGAGNPLGPTQGVGYANELLARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360
QY 361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASASWTVPFAARAYVEMMOCQAEKP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTIVENTQDGFSSAWTVPFASRLYVEMMOCQAEQEP 420
QY 421 LVRVLNDRVYVPLHGCAVDKLGCRKRDDEVEGLSFARSGGNMAECFA 467
Db 421 LVRVLNDRVYVPLHGCPVDALGRCRTDSEFVRLSFARSGGDWAECSFA 467

RESULT 13

US-08-819-825-3
: Sequence 3, Application US/08819825
: Patent No. 5866118
: GENERAL INFORMATION:
: APPLICANT: Berka, Randy M.
: APPLICANT: Ray, Michael W.
: APPLICANT: Klotz, Alan V.
: TITLE OF INVENTION: Polypeptides Having Phytase Activity
: TITLE OF INVENTION: And Nucleic Acids Encoding Same
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 5866118 No. 5866118disk of No. 5866118th America, Inc.
: STREET: 405 Lexington Avenue, Suite 6400
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: FILING DATE: 18-MAR-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambiris, Elias J.
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 4758-200-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 867 0123
: TELEFAX: 212 867 0298
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 467 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-819-825-3

Query Match 76.28; Score 1875; DB 2; Length 467;
Best Local Similarity 75.68; Pred. No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;
QY 1 MGVEVWLLSIATFGSTSGTALGRGNSHSCDVTGQYQCFEISHLWGTYSPYFSLADP 60
Db 1 MGVSAYLLPLLSLGSVTSGLAVPASRNQSSCDIVDQYQCFSETSHLWGOYAPFFSLANE 60

QY 61 SAISPDPVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
Db 51 SVISPEVPACGRVTFPAQVLSRHGARYPTDSKGYKYSALIEIQONATTFDGKYAFLKTYN 120
QY 121 YTLGADDLTPFGENQMVNSGIRFYQRYESLNRNIVPFIIRSSGSRVSIASKKFIEGFQSA 180
Db 121 YSLGADDLTPFGEQELVNSGIRFYQRYESLNRNIVPFIIRSSGSRVSIASKKFIEGFQST 180
QY 181 KLADPGSQPHQASPVINVIIPESGYNNLTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db 181 KLKDPRAQPGQSPKIDVVISSEASSNLTDPGTCTVFEDSELADTVEANFTAFVPSIR 240
QY 241 ARLEADLPQVTLTDEDVYVLMDCPFDTVARTSDATELSPFCALFTHDEWIQDYVLQSLG 300
Db 241 QRLNDLSGVTLTDEVYVLMDCSFDTISTVDTKLSPPFCDLFTHDEWINDYVLQSLK 300
QY 301 KYGYGAGNPLGPAQGVGFANELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db 301 KYGYGAGNPLGPTQGVGYANELLARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360
QY 361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASASWTVPFAARAYVEMMOCQAEKP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTIVENTQDGFSSAWTVPFASRLYVEMMOCQAEQEP 420
QY 421 LVRVLNDRVYVPLHGCAVDKLGCRKRDDEVEGLSFARSGGNMAECFA 467
Db 421 LVRVLNDRVYVPLHGCPVDALGRCRTDSEFVRLSFARSGGDWAECSFA 467

RESULT 14

US-09-163-642-3
: Sequence 3, Application US/09163642
: Patent No. 6221644
: GENERAL INFORMATION:
: APPLICANT: Berka, Randy M.
: APPLICANT: Ray, Michael W.
: APPLICANT: Klotz, Alan V.
: TITLE OF INVENTION: Polypeptides Having Phytase Activity
: TITLE OF INVENTION: And Nucleic Acids Encoding Same
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6221644 No. 6221644disk of No. 6221644th America, Inc.
: STREET: 405 Lexington Avenue, Suite 6400
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: FILING DATE: 18-MAR-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambiris, Elias J.
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 4758-200-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 867 0123
: TELEFAX: 212 867 0298
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 467 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-163-642-3

Query Match 76.2%; Score 1875; DB 3; Length 467;
Best Local Similarity 75.6%; Pred. No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVEVLLSIATLFGSTSGTALPGRNHSCDVTGQYQCFPEISHLWGTYSYPFSLADE 60
DB 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSCDVTGQYQCFSETSHLWQYAPFFSLANE 60

QY 61 SATSPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120
DB 61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGYKSALIEEIQONATTFDGKYAFLKTYN 120

QY 121 YTLGADDLTPFGENOMVNSGKIFRYRYKALARKIVPFIASGSDRVIAAEKPIEGFQSA 180
DB 121 YSLGADDLTPFGEQELVNSGKIFRYVESLTRNIVPFISSGSSRVIASGKKPIEGFQST 180

QY 181 KLADPGSQHOASPVINVIPEGSGYNNITLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLKDPRAQPGQSSPKIDWISEASSNNTLDPGCTVFEDELADTVEANFTATFVPSIR 240

QY 241 ARLEADLPGLVLTDEDVYVLMDCPFDVTARTSDATIELSPFCALFTHDEMIOQDYLOSLG 300
DB 241 QRLENDLSGVILTDTEVYVLMDCSFDTISTVTDIKLSPFCDLFTHDEWINKDYLOSLK 300

QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 KYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

QY 361 HDNMTISIFFALGLYNGTKPLSTTSVESIEETDGYASMTVPFAARAYVEMMOCQAEKEP 420
DB 361 HDNGIISILFALGLYNGTKPLSTTTVENITQIDGFSSANTVPFASRLYVEMMOCQAEQEP 420

QY 421 LVRVLVNDRVVPLHGCVAVDKLGCRKRDDEFGLSFARSGGNWAECEFA 467
DB 421 LVRVLVNDRVVPLHGCVPDAGLGRCTRDSFVRLGSFARSGGDWAECEFA 467

RESULT 15

US-09-233-510-32
Sequence 32, Application US/09233510
Patent No. 6350602
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selzer
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233.510
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-233-510-32

Query Match 76.2%; Score 1875; DB 4; Length 467;
Best Local Similarity 75.6%; Pred. No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVEVLLSIATLFGSTSGTALPGRNHSCDVTGQYQCFPEISHLWGTYSYPFSLADE 60
DB 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSCDVTGQYQCFSETSHLWQYAPFFSLANE 60

QY 61 SATSPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120
DB 61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGYKSALIEEIQONATTFDGKYAFLKTYN 120

QY 121 YTLGADDLTPFGENOMVNSGKIFRYRYKALARKIVPFIASGSDRVIAAEKPIEGFQSA 180
DB 121 YSLGADDLTPFGEQELVNSGKIFRYVESLTRNIVPFISSGSSRVIASGKKPIEGFQST 180

QY 181 KLADPGSQHOASPVINVIPEGSGYNNITLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLKDPRAQPGQSSPKIDWISEASSNNTLDPGCTVFEDELADTVEANFTATFVPSIR 240

QY 241 ARLEADLPGLVLTDEDVYVLMDCPFDVTARTSDATIELSPFCALFTHDEMIOQDYLOSLG 300
DB 241 QRLENDLSGVILTDTEVYVLMDCSFDTISTVTDIKLSPFCDLFTHDEWINKDYLOSLK 300

QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 KYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

QY 361 HDNMTISIFFALGLYNGTKPLSTTSVESIEETDGYASMTVPFAARAYVEMMOCQAEKEP 420
DB 361 HDNGIISILFALGLYNGTKPLSTTTVENITQIDGFSSANTVPFASRLYVEMMOCQAEQEP 420

QY 421 LVRVLVNDRVVPLHGCVAVDKLGCRKRDDEFGLSFARSGGNWAECEFA 467
DB 421 LVRVLVNDRVVPLHGCVPDAGLGRCTRDSFVRLGSFARSGGDWAECEFA 467

Search completed: October 3, 2003, 07:47:49
Job time : 13.9581 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:51 : Search time 106.714 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265B-29
Perfect score: 2462
Sequence: 1 MGVEVLLSLATLFGTSSTG.....DFVEGLSFARSGGNWAECEFA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCI_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2408	97.8	467	14	US-10-083-452-9
2	1875	76.2	467	15	US-10-079-709-32
3	1875	76.2	467	15	US-10-229-358-5
4	1867	75.8	465	14	US-10-083-452-8
5	1867	75.8	465	15	US-10-062-848-78
6	1867	75.8	465	15	US-10-229-358-6
7	1863	75.7	467	14	US-10-083-452-11
8	1860.5	75.6	474	15	US-10-213-990-24
9	1860	75.5	467	9	US-09-929-060-3
10	1859	75.5	465	15	US-10-062-848-80
11	1858	75.5	465	15	US-10-062-848-79
12	1857.5	75.4	439	15	US-10-062-848-3
13	1857.5	75.4	449	15	US-10-062-848-12
14	1855	75.3	465	15	US-10-062-848-81
15	1851	75.2	462	15	US-10-229-358-12

16	1845	74.9	459	15	US-10-062-848-82
17	1835.5	74.6	463	14	US-10-083-452-10
18	1833	74.5	444	15	US-10-062-848-1
19	1820.5	73.9	447	15	US-10-062-848-6
20	1818	73.8	443	9	US-09-929-060-1
21	1813	73.6	443	9	US-09-929-060-2
22	1765	71.7	450	15	US-10-062-848-15
23	1761	71.5	466	14	US-10-083-452-12
24	1761	71.5	466	15	US-10-229-358-7
25	1719	69.8	466	14	US-10-083-452-13
26	1715.5	69.7	450	15	US-10-062-848-9
27	1714	69.6	438	15	US-10-062-848-2
28	1627	66.1	489	15	US-10-229-358-4
29	1627	66.1	489	15	US-10-229-358-10
30	1613	65.5	410	15	US-10-229-358-11
31	1334	54.2	475	14	US-10-083-452-14
32	1313.5	53.4	487	14	US-10-083-452-15
33	1313.5	53.4	487	15	US-10-229-358-8
34	1311	53.2	355	15	US-10-229-358-15
35	1187	48.2	495	14	US-10-083-452-2
36	1182	48.0	478	14	US-10-083-452-3
37	902	36.6	284	15	US-10-229-358-19
38	855	34.7	283	15	US-10-229-358-9
39	855	34.7	283	15	US-10-229-358-24
40	802.5	32.6	443	14	US-10-083-452-5
41	798.5	32.4	439	14	US-10-083-452-7
42	795.5	32.3	453	14	US-10-083-452-6
43	781	31.7	442	14	US-10-083-452-4
44	702.5	28.5	212	15	US-10-229-358-16
45	401	16.3	312	15	US-10-229-358-21

ALIGNMENTS

RESULT 1
US-10-083-452-9
: Sequence 9, Application US/10083452
: Publication No. US20020127218A1
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618.500-US
: CURRENT APPLICATION NUMBER: US/10/083,452
: CURRENT FILING DATE: 2002-02-26
: PRIOR APPLICATION NUMBER: US/09/273,871
: PRIOR FILING DATE: 1999-03-22
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: PRIOR FILING DATE: 1998-06-25
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 467
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 97.8%; Score 2408; DB 14; Length 467;
Best Local Similarity 97.9%; Pred. No. 4.1e-230;
Matches 457; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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DB 1 MGCVFVLLSIATLFGSTSGTALGRGNHSCDVTGQYQCFPEISHLWGTSPYFSLADE 60
QY 61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120
DB 61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGENOMVNSGIKFYRRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 180
DB 121 YTLGADDLTPFGENOMVNSGIKFYRRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 180
QY 181 KLADPGSOPHOASPVINVIPEEGSYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLADPGSOPHOASPVINVIPEEGSYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
QY 241 ARLEADLPGVTLTDEDVYVLMDCPFDTVARTSDATELSPPCALFTHDEWIQYDYIQLSLG 300
DB 241 ARLEADLPGVTLTDEDVYVLMDCPFDTVARTSDATELSPPCALFTHDEWIQYDYIQLSLG 300
QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
QY 361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMCOQAEKEP 420
DB 361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMCOQAEKEP 420
QY 421 LVRVLNDRVVPFHGCAVDKLGRCRDRDFVEGLSFARSGGNWAECEFA 467
DB 421 LVRVLNDRVVPFHGCAVDKLGRCRDRDFVEGLSFARSGGNWAECEFA 467
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RESULT 2

US-10-079-709-32

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; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; SOFTWARE: Patent in Release #1.0, Version #1.25
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-079-709-32
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Query Match 76.2%; Score 1875; DB 15; Length 467;

Best Local Similarity 75.6%; Pred. No. 3.4e-177; Indels 0; Gaps 0;

Matches 553; Conservative 41; Mismatches 73;

QY 1 MGCVFVLLSIATLFGSTSGTALGRGNHSCDVTGQYQCFPEISHLWGTSPYFSLADE 60

DB 1 MGCVFVLLSIATLFGSTSGTALGRGNHSCDVTGQYQCFPEISHLWGTSPYFSLADE 60

QY 61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120

DB 61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120

QY 121 YTLGADDLTPFGENOMVNSGIKFYRRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 180

DB 121 YTLGADDLTPFGENOMVNSGIKFYRRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 180

QY 181 KLADPGSOPHOASPVINVIPEEGSYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240

DB 181 KLADPGSOPHOASPVINVIPEEGSYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240

QY 241 ARLEADLPGVTLTDEDVYVLMDCPFDTVARTSDATELSPPCALFTHDEWIQYDYIQLSLG 300

DB 241 ARLEADLPGVTLTDEDVYVLMDCPFDTVARTSDATELSPPCALFTHDEWIQYDYIQLSLG 300

QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

DB 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

QY 361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMCOQAEKEP 420

DB 361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMCOQAEKEP 420

QY 421 LVRVLNDRVVPFHGCAVDKLGRCRDRDFVEGLSFARSGGNWAECEFA 467

DB 421 LVRVLNDRVVPFHGCAVDKLGRCRDRDFVEGLSFARSGGNWAECEFA 467

RESULT 3

US-10-229-358-5

; Sequence 5, Application US/10229358

; Publication No. US20030124700A1

; GENERAL INFORMATION:

; APPLICANT: Stafford, Christian F.

; APPLICANT: Trinci, Anthony P.J.

; APPLICANT: Brookman, Jayne L.

; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding

; FILE REFERENCE: GC586-2

; CURRENT APPLICATION NUMBER: US/10/229,358

; CURRENT FILING DATE: 2002-08-26

; PRIOR APPLICATION NUMBER: US 60/148,960

; PRIOR FILING DATE: 1999-08-13

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 467

; TYPE: PRI

; ORGANISM: Aspergillus niger

US-10-229-358-5

Query Match 76.2%; Score 1875; DB 15; Length 467;

Best Local Similarity 75.6%; Pred. No. 3.4e-177;

QY 421 LVRVLNDRVPLHGCADKLGCRCKRDDVEGLSFARSGGNNAECFA 467
DB 421 LVRVLNDRVPLHGCPCVDALGRCTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 8

US-10-213-990-24
; Sequence 24, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213.990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-24

Query Match 75.6%; Score 1860.5; DB 15; Length 474;
Best Local Similarity 75.3%; Pred. No. 9.5e-176;
Matches 351; Conservative 41; Mismatches 67; Indels 7; Gaps 2;

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DB 16 GAVVLLKRSVSAAPSS-----AGSKSCDVTDLGYOCSPATSHLWGYSPYFSLADEL 69
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DB 70 SVSSKLPKDCRITLVQVLSRHGARYPTSSSKKYYKLVTAIQANATDFKGFALUKTYN 123
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DB 130 TLGADDLTPFGEOQLVNSGKIFRYRYKALARKIVPFIRASGSDRVIASAEKFIQFQSAK 189
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DB 190 LADFGA-TNRAAPALSVILIPSEIFENNTLDHGVCTKFEASCGDVEANFTALFAPAIRA 248
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DB 249 RAEXHLPGVTLTDEDVYLMDCMCFDVTARTSDASQLSPFCOLFTHNEWKYNYLQSLGK 308
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DB 309 YGYGAGNPLGPAQGIPTNLSIARLTHSPVQDHTSTNHLSDSNPATFPLNATLYADFSH 368
QY 362 DNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASMTVPFAARAYVEMMCOCAKEPL 421
DB 369 DNSWVSIFFALGLYNGTEPLSRTSVESAKELDGYASWVVPFGARAYFETNQCCKEPL 428
QY 422 VRLVNDRVVPLHGCADKLGCRCKRDDVEGLSFARSGGNNAECFA 467
DB 429 VRLVNDRVVPLHGCADKLGCRCKLNDVFKGLSFARSGGNNGECFS 474

RESULT 9

US-09-929-060-3
; Sequence 3, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIDEWASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI

; APPLICANT: JANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929.060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-929-060-3

Query Match 75.5%; Score 1860; DB 9; Length 467;
Best Local Similarity 74.1%; Pred. No. 1e-175;
Matches 346; Conservative 48; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVEVVLLSTATLFGSTGTALGPRGNHSCDVTGGYOCPEISHLWCTGYSPYFSLADE 60
DB 1 MGVSALLPLLYLLSGVTSLGLAVPASRNQSTCDTVDQGYOCFSETSHLWGYAPFFSLANK 6C
QY 61 SAISPDPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAPKGYAFUKTYN 120
DB 61 SAISPDPVAGCHVTFAQVLSRHGARYPTDSKGGKYSALIEIQONATTFEGKYAFUKTYN 120
QY 121 YTLGADDLTPFGENOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIASAEKFIQFQSA 180
DB 121 YSLGADDLTPFGEOQLVNSGKIFRYRYKALARKIVPFIRASGSDRVIASGNKFIQFQST 180
QY 181 KLADPGSOPHOASPVNIVTIPESGYNNITLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLADPRAQCOSSPKIDVIVISEASTSNNTLDGCTVFEDELADIEANFTATFVPSIR 240
QY 241 ARLEADLPQVTLTDEDVYLMDCMCPDVTARTSDATELSPPFCALFTHDEWIQDYLOSJG 300
DB 241 QRLNDLSGVSLTDEVTYLMDCMCFDITSTSDTKLSPFCDLFTHDEWINDYLOSJN 300
QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHLSDSNPATFPLNATLYADF 360
DB 301 KYTGHGAGNPLGPIQGVGFANELIARLTHSPVHDDTSSNHLSDSNPATFPLNATLYADF 360
QY 361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASMTVPFAARAYVEMMCOCAKEP 420
DB 361 HDNGIISILFALGLYNGTKPLSSTTAENITQTDGFSAMTVPFASRMVEMMCOQSEQP 420
QY 421 LVRVLNDRVPLHGCADKLGCRCKRDDVEGLSFARSGGNNAECFA 467
DB 421 LVRVLNDRVPLHGCPCVDALGRCTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 10

US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062.848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19

1

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QY 88 TSSASKAYSALIEAIQKNATAFKGYAFELKTYNTYTLGADDLIPFGENQMVNSGZKFTYRY 147
DB 61 ISSKSKYKLVTAIOANATDFKGFALKTNYTLGADDLIPFGEQQLVNSGKIFCYRY 120
QY 148 KALARKIVPFIASSSDRVIAAEKFIQFQSAKLADPGSQPHQASPVINVIIPGSGYN 207
DB 121 KALARSVPFIASSSDRVIAAEKFIQFQSAKLADPGCA-TNRAAPALSVIIPSEIFN 179
QY 208 NTLDHGCTAFEDSELGDDVEANFTALFAPAIRARLEADLPQVTLTDEDVYVLMQCPFD 267
DB 180 NTLDHGCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVYVLMQCSFD 239
QY 268 TVARTSDATELSPFCALFTHDEWIQYDXLQSLGKYYGYGAGNPLGPAQGVGFANELIARL 327
DB 240 TVARTSDASQLSPFCOLFTHNEWKKNYVLSQSLGKYYGYGAGNPLGPAQGVGFANELIARL 299
QY 328 THSPVQDHTSTNHTLDSNPATPLNATLYADFSHONTMISIFFALGLYNGTKPLSTTSVE 387
DB 300 TRSPVQDHTSTNHTLDSNPATPLNATLYADFSHONSVMYSIFFALGLYNGTEPLSRISVE 359
QY 388 SIETDGYASMTVPFAARAYVEMMOCAKEBPLVRLVNDRVVPLHGCADVDKLGRCKRD 447
DB 360 SAKELDGYASWVYPGARAYFETMOCKSEKBPVLRALINDRVVPLHGCADVDKLGRCKLN 419
QY 448 DFVEGLSFARSGGNWAECEFA 467
DB 420 DFVKGLSWARSGGNWGECEFS 439

RESULT 13
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.5
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Query Match 75.4%; Score 1857.5; DB 15; Length 449;
Best Local Similarity 78.9%; Pred. No. 1-7e-175;
Matches 347; Conservative 36; Mismatches 56; Indels 1; Gaps 1;

QY 28 SHSCDVTGQYQCFEISHLWGTYSYFSLADESAISPDVDCRVTFVQVLSRHGARYP 87
DB 11 SKSCDVTDLGQCPATSHLWGOYSPFSELSVSKLPKDCRITLVQVLSRHGARYP 70
QY 88 TSSASKAYSALIEAIQKNATAFKGYAFELKTYNTYTLGADDLIPFGENQMVNSGKIFYRY 147
DB 71 TSSKSKYKLVTAIOANATDFKGFALKTNYTLGADDLIPFGEQQLVNSGKIFCYRY 130
QY 148 KALARKIVPFIASSSDRVIAAEKFIQFQSAKLADPGSQPHQASPVINVIIPGSGYN 207
DB 131 KALARSVPFIASSSDRVIAAEKFIQFQSAKLADPGCA-TNRAAPALSVIIPSEIFN 189
QY 208 NTLDHGCTAFEDSELGDDVEANFTALFAPAIRARLEADLPQVTLTDEDVYVLMQCPFD 267
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DB 190 NTLDHGCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVYVLMQCSFD 249
QY 268 TVARTSDATELSPFCALFTHDEWIQYDXLQSLGKYYGYGAGNPLGPAQGVGFANELIARL 327
DB 250 TVARTSDASQLSPFCOLFTHNEWKKNYVLSQSLGKYYGYGAGNPLGPAQGVGFANELIARL 309
QY 328 THSPVQDHTSTNHTLDSNPATPLNATLYADFSHONTMISIFFALGLYNGTKPLSTTSVE 387
DB 310 TRSPVQDHTSTNHTLDSNPATPLNATLYADFSHONSVMYSIFFALGLYNGTEPLSRISVE 369
QY 388 SIETDGYASMTVPFAARAYVEMMOCAKEBPLVRLVNDRVVPLHGCADVDKLGRCKRD 447
DB 370 SAKELDGYASWVYPGARAYFETMOCKSEKBPVLRALINDRVVPLHGCADVDKLGRCKLN 429
QY 448 DFVEGLSFARSGGNWAECEFA 467
DB 430 DFVKGLSWARSGGNWGECEFS 449

RESULT 14
US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.5
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Query Match 75.3%; Score 1855; DB 15; Length 465;
Best Local Similarity 75.6%; Pred. No. 3.2e-175;
Matches 353; Conservative 37; Mismatches 75; Indels 2; Gaps 2;

QY 1 MGVFVVLSIATLFGSTSGTALGPRGNSHSCDVTGQYQCFEISHLWGTYSYFSLADE 60
DB 1 MVTTLFVLSAAYLLSGRVSAAPSAG-SKSCDVTDLGQYQCPATSHLWGOYSPFSELE 59
QY 61 SAISPDPVDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFELKTYN 120
DB 60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKYKLVTAIOANATDFKGFALKTYN 119
QY 121 YTLGADDLTPFGENQMVNSGKIFYRYKALARKIVFPIRASSGSDRVIAAEKFIQFQSA 180
DB 120 YTLGADDLTPFGEQQLVNSGKIFCYRYKALARSVPFIASSGSDRVIAAEKFIQFQSA 179
QY 181 KLADPGSQPHQASPVINVIIPGSGYNNTLDHCTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 180 KLADPGCA-TNRAAPALSVIIPSEIFNTNLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238
QY 241 ARLEADLPQVTLTDEDVYVLMQCPEDTVARTSDATELSPFCALFTHDEWIQYDXLQSLG 300
DB 239 ARAKHLPGVTLTDEDVYVLMQCSFDTVARTSDASQLSPFCOLFTHNEWKKNYVLSQSLG 298
QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADEFS 360
DB 300 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADEFS 360
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Db      299 KYGYGACNPLGPAQIGIFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYDFS 358
QY      361 HDNTMISIFFALGLYNGTKPLSTISVSIESIETDGYASASHTVPPFAARAYVEMMQOAEKEP 420
Db      359 HDNSMYSIFFALGLYNGTEPLSRSTVSASAKELDGYASAWVYPFGARAYFETMOCKSEKEP 418
QY      421 LVRVLNDRVVPPLHGCAVDKLGCRCKRDEVEGLSFARSGGNWAECEFA 467
Db      419 LVRALINDRVVPLHGCDVDKLGCRCKLNDFKVGLSWARSGGNWGECEFS 465

RESULT 15
US-10-229-358-12
: Sequence 12, Application US/10229358
: Publication NO. US20030124700A1
: GENERAL INFORMATION:
: APPLICANT: Stafford, Christian F.
: APPLICANT: Trinci, Anthony P.J.
: APPLICANT: Brookman, Jayne L.
: TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
: TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
: FILE REFERENCE: GC586-2
: CURRENT APPLICATION NUMBER: US/10/229,358
: CURRENT FILING DATE: 2002-08-26
: PRIOR APPLICATION NUMBER: US 60/148,960
: PRIOR FILING DATE: 1999-08-13
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 12
: LENGTH: 462
: TYPE: PRT
: ORGANISM: Aspergillus niger
US-10-229-358-12

Query Match      75.2%      Score 1851: DB 15: Length 462:
Best Local Similarity 75.5%: Pred. No. 8e-175:
Matches 349: Conservative 41: Mismatches 72: Indels 0: Gaps 0:

QY      1  MGVEVLLSIATLFGSTGALGPRGNSHSDTVDGGYOCFPEISHLWGTYSVPYFSLADE 60
Db      1  MGVSALLPLLYLLSGVTSLAVPASRNSSCDTVDGYOCFSETSHLWGYAPFESLANE 60
QY      61  SAISPVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
Db      61  SVISPEVPAGCRVTPAQVLSRHGARYPTDSKGYKYSALIEEIQONATTFDGKYAFLKTYN 120
QY      121 YTLGADDLTPFCENOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIASAEKFTIEGFOSA 180
Db      121 YSLGADDLTPFGEQELVNSGKIFQRYESLRTNIVPFISSGSSRVIASGKKFIEGFQST 180
QY      181 KLADPGSQPHQASPVINVTIPGSGYNNTLDHGCTAFEDSELGDDVEANFTALFAPAIR 240
Db      181 KLMDPRAQPGQSSPKIDVYISEASSSNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240
QY      241 ARLEADLPGVTLTDEDVYVLDMDCPDTPARTSDATELSPFCAFTHDEWIQYDYLOS LG 300
Db      241 QRLNDLSGVTLTDEVTYVLDMDCSFDLTISTVDTKLSPCDFTHDEWINYDYLOSLK 300
QY      301 KYGYGACNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db      301 KYGYHGACNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360
QY      361 HDNTMISIFFALGLYNGTKPLSTISVSIESIETDGYASASHTVPPFAARAYVEMMQOAEKEP 420
Db      361 HDNGIISILFALGLYNGTKPLSTTTTITENITQDGFSSANTVPPFASRLYVEMMQOAEKEP 420
QY      421 LVRVLNDRVVPPLHGCAVDKLGCRCKRDEVEGLSFARSGGNW 462
Db      421 LVRVLNDRVVPPLHGCFVDALGCRCTRDSFVRGLSFARSGGDW 462
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Search completed: October 3, 2003, 08:12:30
Job time : 107.714 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: October 3, 2003, 07:46:51 ; Search time 106.774 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265B-31

Perfect score: 2468
Sequence: 1 MGVFVLLSLATLFGTSST.....DFVEGLSPARSGGNWEECA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pcp.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2308	93.5	467	14	US-10-083-452-9
2	1888	76.5	465	14	US-10-083-452-8
3	1888	76.5	465	15	US-10-062-848-78
4	1888	76.5	465	15	US-10-229-358-6
5	1881.5	76.2	474	15	US-10-213-990-24
6	1880	76.2	465	15	US-10-062-848-80
7	1879	76.1	465	15	US-10-062-848-79
8	1878.5	76.1	439	15	US-10-062-848-3
9	1878.5	76.1	449	15	US-10-062-848-12
10	1876	76.0	465	15	US-10-062-848-81
11	1854	75.1	469	15	US-10-062-848-82
12	1848	74.9	467	15	US-10-079-709-32
13	1848	74.9	467	15	US-10-229-358-5
14	1841	74.6	467	9	US-09-929-060-3
15	1836	74.4	467	14	US-10-083-452-11

16	1829	74.1	462	15	US-10-229-358-12
17	1806	73.2	444	15	US-10-062-848-1
18	1804.5	73.1	463	14	US-10-083-452-10
19	1799	72.9	443	9	US-09-929-060-1
20	1794	72.7	443	9	US-09-929-060-2
21	1789.5	72.5	447	15	US-10-062-848-6
22	1752	71.0	466	14	US-10-083-452-12
23	1752	71.0	466	15	US-10-229-358-7
24	1748	70.8	450	15	US-10-062-848-15
25	1710	69.3	466	14	US-10-083-452-13
26	1706.5	69.1	450	15	US-10-062-848-9
27	1697	68.6	438	15	US-10-062-848-2
28	1658	67.2	489	15	US-10-229-358-4
29	1658	67.2	489	15	US-10-229-358-10
30	1623	65.8	410	15	US-10-229-358-11
31	1381	56.0	475	14	US-10-083-452-14
32	1339	54.3	355	15	US-10-229-358-15
33	1334.5	54.1	487	14	US-10-083-452-15
34	1334.5	54.1	487	15	US-10-229-358-8
35	1215	49.2	495	14	US-10-083-452-2
36	1210	49.0	478	14	US-10-083-452-3
37	920	37.3	284	15	US-10-229-358-19
38	867	35.1	283	15	US-10-229-358-9
39	867	35.1	283	15	US-10-229-358-24
40	845.5	34.3	443	14	US-10-083-452-5
41	833.5	33.8	453	14	US-10-083-452-6
42	830.5	33.7	439	14	US-10-083-452-7
43	825	33.4	442	14	US-10-083-452-4
44	729.5	29.6	212	15	US-10-229-358-16
45	406	16.5	312	15	US-10-229-358-21

ALIGNMENTS

RESULT 1

US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.50G-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273.871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 004C7
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080.129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/050.675
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 93.5%; Score 2308; DB 14; Length 467;
Best Local Similarity 93.4%; Pred. No. 6.9e-224;
Matches 436; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLPGSTGCTALGPRGNHSCDVTVDGGVQCPEIISHLWGTYSPPFSLADE 60
Db 1 MGVFVLLSIATLPGSTGCTALGPRGNHSCDVTVDGGVQCPEIISHLWGTYSPPFSLADE 60
QY 61 SAISPDVPKGCRTVTVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
Db 61 SAISPDVPKGCRTVTVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOQA 180
Db 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOQA 180
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGCTAFESSELGDDVEANFTAVFAPPIR 240
Db 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGCTAFESSELGDDVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNTLDEVDVNLMDMCPFDVARTSDATQSPFCDLFTHDENQYDYLOSLS 300
Db 241 ARLEAHLPGVNTLDEVDVNLMDMCPFDVARTSDATQSPFCDLFTHDENQYDYLOSLS 300
QY 301 KYGYGAGNPLGPAOGVGFVNELIARLTHSPVQDHTSTNNHILDSNPATFPLNATLYADF 360
Db 301 KYGYGAGNPLGPAOGVGFVNELIARLTHSPVQDHTSTNNHILDSNPATFPLNATLYADF 360
QY 361 HONTMYSIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVENMOCQAEKEP 420
Db 361 HONTMYSIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVENMOCQAEKEP 420
QY 421 LVRVLNDRVPLHGGGVKLCRCRDDFVEGLSFARSGGNWEECEFA 467
Db 421 LVRVLNDRVPLHGGGVKLCRCRDDFVEGLSFARSGGNWEECEFA 467

RESULT 2

US-10-083-452-8

; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus

US-10-083-452-8

Query Match 76.5%; Score 1888; DB 14; Length 465;
Best Local Similarity 76.9%; Pred. No. 1.6e-181;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLPGSTGCTALGPRGNHSCDVTVDGGVQCPEIISHLWGTYSPPFSLADE 60
Db 1 MVTLTLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGTYSPPFSLADE 59

QY 61 SAISPDVPKGCRTVTVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
Db 61 LSVSSKLPKDCRITLTVQLSRHGARYPTSSSKKYYKLVTAIQANATDFKGF AFLKTYN 119
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOQA 180
Db 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOQA 179
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGCTAFESSELGDDVEANFTAVFAPPIR 240
Db 181 KLADPGAT-NRAAPATSVIIESETFNNTLDHGCTFEASQLGDEVAANFTALFAPDIR 238
QY 241 ARLEAHLPGVNTLDEVDVNLMDMCPFDVARTSDATQSPFCDLFTHDENQYDYLOSLS 300
Db 239 ARAEKLPGVTLTDEVDVNLMDMCSFDVARTSDASQLSPFCOLFTHNEWKYYNYLQSLG 298
QY 301 KYGYGAGNPLGPAOGVGFVNELIARLTHSPVQDHTSTNNHILDSNPATFPLNATLYADF 360
Db 299 KYGYGAGNPLGPAOGIGFTNELIARLTHSPVQDHTSTNNHILDSNPATFPLNATLYADF 358
QY 361 HONTMYSIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVENMOCQAEKEP 420
Db 359 HONSMYSIFFALGLYNGTEPLSRSTSVESAKELDGYASWVVPFGARAYFETMOCKSEKEP 418
QY 421 LVRVLNDRVPLHGGGVKLCRCRDDFVEGLSFARSGGNWEECEFA 467
Db 419 LVRALINDRVVPLHCCDVKLCRCRDLNDFVKLSWAKSGGNWEECEFS 465

RESULT 3

US-10-062-848-78

; Sequence 78, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus

US-10-062-848-78

Query Match 76.5%; Score 1888; DB 15; Length 465;
Best Local Similarity 76.9%; Pred. No. 1.6e-181;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLPGSTGCTALGPRGNHSCDVTVDGGVQCPEIISHLWGTYSPPFSLADE 60
Db 1 MVTLTLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGTYSPPFSLADE 59
QY 61 SAISPDVPKGCRTVTVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
Db 60 LSVSSKLPKDCRITLTVQLSRHGARYPTSSSKKYYKLVTAIQANATDFKGF AFLKTYN 119
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOQA 180
Db 120 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOQA 179
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGCTAFESSELGDDVEANFTAVFAPPIR 240


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; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-80

Query Match 76.2%; Score 1880; DB 15; Length 465;
Best Local Similarity 76.7%; Pred. No. 1.1e-180;
Matches 358; Conservative 35; Mismatches 72; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGTALGPRGNHSCDIYDGGYQCFFPEISHLWGTYSPPFSLADE 60
DB 1 MVTLLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQYSPFFSLEDE 59

QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFKLTYN 120
DB 60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSASKYKLVTAIOANATDFKGFALFKTYN 119

QY 121 YTLGADDLTPFEGQOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIASAEKIEGFQSA 180
DB 120 YTLGADDLTPFEGQOLVNSGKIFRYRYKALARSVVPFIRASGSDRVIASAEKIEGFQQA 179

QY 181 KLAOPGANPHOASPVNVIPEGAGYNNLTLDHGLCTAFESSELGDDVEANFTAVFAPP 240
DB 180 KLAOPGANPHOASPVNVIPEGAGYNNLTLDHGLCTAFESSELGDDVEANFTAVFAPP 238

QY 241 ARLEAHLPGVNLTDDEVVSLMDMCFDVTARTSDATOLSPFCDLFTHDENIOTDYLOS 300
DB 239 ARAEKHLPGVNLTDDEVVSLMDMCFDVTARTSDATOLSPFCDLFTHDENIOTDYLOS 298

QY 301 KYGYGAGNPLGPAOGVGVNELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADF 360
DB 299 KYGYGAGNPLGPAOGVGVNELLARLTHSPVQDHTSTNHTLDSNPATFPLNATMYVDF 358

QY 361 HDNTMVSIFPFGALGLYNGTKPLSTTSVESIETDGYASWTVPFAARAYVENMOCEAKEP 420
DB 359 HDNTMVSIFPFGALGLYNGTKPLSTTSVESIETDGYASWTVPFAARAYFETMOCKSEK 418

QY 421 LVRVLNDRVPLHCGGVKLGRCRKRODFVEGLSFARSGGNWCECFA 467
DB 419 LVRALINDRVVPLHCGCDVDKLGRCRKLNDFVKGLSWARSGGNWCECFS 465

RESULT 7
US-10-062-848-79
; Sequence 79, Application US/10062848
; Publication NO. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREMA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus

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; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-79

Query Match 76.1%; Score 1879; DB 15; Length 465;
Best Local Similarity 76.7%; Pred. No. 1.3e-180;
Matches 358; Conservative 35; Mismatches 72; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGTALGPRGNHSCDIYDGGYQCFFPEISHLWGTYSPPFSLADE 60
DB 1 MVTLLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQYSPFFSLEDE 59

QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFKLTYN 120
DB 60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSASKYKLVTAIOANATDFKGFALFKTYN 119

QY 121 YTLGADDLTPFEGQOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIASAEKIEGFQSA 180
DB 120 YTLGADDLTPFEGQOLVNSGKIFRYRYKALARSVVPFIRASGSDRVIASAEKIEGFQQA 179

QY 181 KLAOPGANPHOASPVNVIPEGAGYNNLTLDHGLCTAFESSELGDDVEANFTAVFAPP 240
DB 180 KLAOPGANPHOASPVNVIPEGAGYNNLTLDHGLCTAFESSELGDDVEANFTAVFAPP 238

QY 241 ARLEAHLPGVNLTDDEVVSLMDMCFDVTARTSDATOLSPFCDLFTHDENIOTDYLOS 300
DB 239 ARAEKHLPGVNLTDDEVVSLMDMCFDVTARTSDATOLSPFCDLFTHDENIOTDYLOS 298

QY 301 KYGYGAGNPLGPAOGVGVNELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADF 360
DB 299 KYGYGAGNPLGPAOGVGVNELLARLTHSPVQDHTSTNHTLDSNPATFPLNATMYVDF 358

QY 361 HDNTMVSIFPFGALGLYNGTKPLSTTSVESIETDGYASWTVPFAARAYVENMOCEAKEP 420
DB 359 HDNTMVSIFPFGALGLYNGTKPLSTTSVESIETDGYASWTVPFAARAYFETMOCKSEK 418

QY 421 LVRVLNDRVPLHCGGVKLGRCRKRODFVEGLSFARSGGNWCECFA 467
DB 419 LVRALINDRVVPLHCGCDVDKLGRCRKLNDFVKGLSWARSGGNWCECFS 465

RESULT 8
US-10-062-848-3
; Sequence 3, Application US/10062848
; Publication NO. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREMA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus

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US-10-062-848-3

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Query Match 76.1%; Score 1878.5; DB 15; Length 439;
Best Local Similarity 79.8%; Pred. No. 1.4e-180;
Matches 351; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

Qy 28 SHSCDTVDGGYQCFEISHLWGTYSFFSFLADESAISPDVPGKGRVTFVQVLSRHGARYP 87
Db 1 SKSCDTVDLGYQCPATSHLWQYSPFFSLEDELSVSKLPKDCRITLVQVLSRHGARYP 60

Qy 88 TSSASKAYSALIEAIQKNATAPFKGYAFKTYNTLGCADLTLPFGEOQVMVNSGIKFRYR 147
Db 61 TSSKSKYKKLVTAIQANATDFKGFALFKTYNTLGCADLTLPFGEOQVMVNSGIKFRYR 120

Qy 148 KALARKIVPPIRASGSDRVIASAEKFTIEGFSQAKLADPGANPHQASPVNVIPEGAGYN 207
Db 121 KALARSVVPPIRASGSDRVIASAEKFTIEGFSQAKLADPGAT-NKAAPASVVIPESEIEN 179

Qy 208 NTLDHGLCTAFESSELGDVEANFTAVFAPPIRARLEAHLPGVNLTDVWNLMDMCPED 267
Db 180 NTLDHGVTCTFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEWVSLMDMCSFD 239

Qy 268 TVARTSDATOLSPCCDLFTHEMIQDYLOSLOKYYGYGAGNPLGPAQGVGFVNELIARL 327
Db 240 TVARTSDASLSPCCQLFTHEMKKYNLOSLOKYYGYGAGNPLGPAQGIQFTNELIARL 299

Qy 328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMYSIFFALGLYNGTKPLSTTSVE 387
Db 300 TRSPVQDHTSTNLTSLVSNPATFPLNATMYVDFSHDNSHWSIFFALGLYNGTEPLSTTSVE 359

Qy 388 SIEETDGYASWTVPFAARAYVENMOCEAEKPELVRVLRVNDRVVPLRGGVQDKLGRCK3D 447
Db 360 SAKELDGYASWVVPFGARAYFETMCKSEKPELVRALINDRVVPLRGCDVDKGRCKLN 419

Qy 448 DFVEGLSFARSGGNWECFA 467
Db 420 DFVKGLSWARSGGNWECFS 439

RESULT 9
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US2003092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Query Match 76.1%; Score 1878.5; DB 15; Length 449;
Best Local Similarity 79.8%; Pred. No. 1.4e-180;
Matches 351; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

Qy 28 SHSCDTVDGGYQCFEISHLWGTYSFFSFLADESAISPDVPGKGRVTFVQVLSRHGARYP 87
Db 11 SKSCDTVDLGYQCPATSHLWQYSPFFSLEDELSVSKLPKDCRITLVQVLSRHGARYP 70
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Qy 88 TSSASKAYSALIEAIQKNATAPFKGYAFKTYNTLGCADLTLPFGEOQVMVNSGIKFRYR 147
Db 71 TSSKSKYKKLVTAIQANATDFKGFALFKTYNTLGCADLTLPFGEOQVMVNSGIKFRYR 130

Qy 148 KALARKIVPPIRASGSDRVIASAEKFTIEGFSQAKLADPGANPHQASPVNVIPEGAGYN 207
Db 131 KALARSVVPPIRASGSDRVIASAEKFTIEGFSQAKLADPGAT-NRAAPASVVIPESEIEN 189

Qy 208 NTLDHGLCTAFESSELGDVEANFTAVFAPPIRARLEAHLPGVNLTDVWNLMDMCPED 267
Db 190 NTLDHGVTCTFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEWVSLMDMCSFD 249

Qy 268 TVARTSDATOLSPCCDLFTHEMIQDYLOSLOKYYGYGAGNPLGPAQGVGFVNELIARL 327
Db 250 TVARTSDASLSPCCQLFTHEMKKYNLOSLOKYYGYGAGNPLGPAQGIQFTNELIARL 309

Qy 328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMYSIFFALGLYNGTKPLSTTSVE 387
Db 310 TRSPVQDHTSTNLTSLVSNPATFPLNATMYVDFSHDNSHWSIFFALGLYNGTEPLSTTSVE 369

Qy 388 SIEETDGYASWTVPFAARAYVENMOCEAEKPELVRVLRVNDRVVPLRGGVQDKLGRCKRD 447
Db 370 SAKELDGYASWVVPFGARAYFETMCKSEKPELVRALINDRVVPLRGCDVDKGRCKLN 429

Qy 448 DFVEGLSFARSGGNWECFA 467
Db 430 DFVKGLSWARSGGNWECFS 449

RESULT 10
US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US2003092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Query Match 76.0%; Score 1876; DB 15; Length 465;
Best Local Similarity 76.4%; Pred. No. 2.7e-180;
Matches 357; Conservative 36; Mismatches 72; Indels 2; Gaps 2;

Qy 1 MGVFVVLISLTIATLFGSTSGTALGPRGNHSCDVTVDGGYQCFEISHLWGTYSFFSFLADE 60
Db 1 MVTLTFLLSAAYLLSGRVSAAAPSSAG-SKSCDTVDLGYQCPATSHLWQYSPFFSLEDE 59

Qy 61 SAISPDVPGKGRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAPFKGYAFKTYN 120
Db 60 LSVSKLPEKDCRITLVQVLSRHGARYPTSSKSKYKKLVTAIQANATDFKGFALFKTYN 119

Qy 121 YTLGADDLTPFGEOQVMVNSGIKFRYRVRKALARKIVPPIRASGSDRVIASAEKFTIEGFSQA 180
Db 120 YTLGADDLTAFGEQQLVNSGIKFRYQRYKALARSVVPPIRASGSDRVIASAEKFTIEGFSQA 179
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Db 61 SVLSPEVPAGCRVYTFQAQVLSRHGARYPTDSKCKKYSALIEEQNATIEDGKYAFKLTYN 120
QY 121 YTLGADDLTPFGQQQMVNSGKIFRYRYKALARKIVPFIASGSDRVIASAEKFIIEGFQSA 180
Db 121 YSLGADDLTPFGQELVNSGKIFRYQYESLTRNIVPFISSGSSRVIASGKKFIEGFQST 180
QY 181 KLADPGANPHQASPVINVIIEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLADPRAQPGQSSPKIDVWISSEASSNNTLDPGCTVFEDSELADTVEANFTAVFVPSIR 240
QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPDVTARTSDATQLSPFCDLFTHDEWIDYQLQSLG 300
Db 241 ORLENDLSGVTLTDEVTYILMDMCSFDTISTSTVDTKLSFPCDLFTHDEWINDYQLQSLK 300
QY 301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVODHTSTNHTLDSNPAIFPLNATLYADFS 360
Db 301 KYYGAGNPLGPTQGVGYANELLARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360
QY 361 HDNTMVSIFPAGLNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMOCEAKEP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSASWTVPFASRLYVEMMOCEAQEP 420
QY 421 LVRVLVNDRVVPLHGGCVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db 421 LVRVLVNDRVVPLHGGCPVDALGRCTRDSFVRGLSFARSGGDWAECPA 467

RESULT 13
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trincl, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-229-358-5

Query Match 74.9%; Score 1848; DB 15; Length 467;
Best Local Similarity 74.3%; Prod. No. 1.8e-177;
Matches 347; Conservative 42; Mismatches 78; Indels 0; Gaps 0;

QY 1 MGWVWLLSTATLFGSTGTALGPRGNSCOTVDGQYQCFPEISHLWGTYSFFTSIADE 60
Db 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSCOTVDQYQCFSEISHLWGOYAPFSLANE 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSAKAYSALIEAOKNATAFKGYAFKLTYN 120
Db 61 SVLSPEVPAGCRVYTFQAQVLSRHGARYPTDSKCKKYSALIEEQNATIEDGKYAFKLTYN 120
QY 121 YTLGADDLTPFGQQQMVNSGKIFRYRYKALARKIVPFIASGSDRVIASAEKFIIEGFQSA 180
Db 121 YSLGADDLTPFGQELVNSGKIFRYQYESLTRNIVPFISSGSSRVIASGKKFIEGFQST 180
QY 181 KLADPGANPHQASPVINVIIEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLADPRAQPGQSSPKIDVWISSEASSNNTLDPGCTVFEDSELADTVEANFTAVFVPSIR 240
QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPDVTARTSDATQLSPFCDLFTHDEWIDYQLQSLG 300
Db 241 ORLENDLSGVTLTDEVTYILMDMCSFDTISTSTVDTKLSFPCDLFTHDEWINDYQLQSLK 300
QY 301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVODHTSTNHTLDSNPAIFPLNATLYADFS 360
Db 301 KYYGAGNPLGPTQGVGYANELLARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360
QY 361 HDNTMVSIFPAGLNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMOCEAKEP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSASWTVPFASRLYVEMMOCEAQEP 420
Db 241 ORLENDLSGVTLTDEVTYILMDMCSFDTISTSTVDTKLSFPCDLFTHDEWINDYQLQSLK 300
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QY 301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVODHTSTNHTLDSNPAIFPLNATLYADFS 360
Db 301 KYYGAGNPLGPTQGVGYANELLARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360
QY 361 HDNTMVSIFPAGLNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMOCEAKEP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSASWTVPFASRLYVEMMOCEAQEP 420
QY 421 LVRVLVNDRVVPLHGGCVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db 421 LVRVLVNDRVVPLHGGCPVDALGRCTRDSFVRGLSFARSGGDWAECPA 467

RESULT 14
US-09-929-060-3
; Sequence 3, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIDEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-929-060-3

Query Match 74.6%; Score 1841; DB 9; Length 467;
Best Local Similarity 73.2%; Prod. No. 9.1e-177;
Matches 342; Conservative 49; Mismatches 76; Indels 0; Gaps 0;

QY 1 MGWVWLLSTATLFGSTGTALGPRGNSCOTVDGQYQCFPEISHLWGTYSFFTSIADE 60
Db 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSCOTVDQYQCFSEISHLWGOYAPFSLANE 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSAKAYSALIEAOKNATAFKGYAFKLTYN 120
Db 61 SAISPDVPAGCRVYTFQAQVLSRHGARYPTDSKCKKYSALIEEQNATIEDGKYAFKLTYN 120
QY 121 YTLGADDLTPFGQQQMVNSGKIFRYRYKALARKIVPFIASGSDRVIASAEKFIIEGFQSA 180
Db 121 YSLGADDLTPFGQELVNSGKIFRYQYESLTRNIVPFISSGSSRVIASGKKFIEGFQST 180
QY 181 KLADPGANPHQASPVINVIIEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLADPRAQPGQSSPKIDVWISSEASSNNTLDPGCTVFEDSELADTVEANFTAVFVPSIR 240
QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPDVTARTSDATQLSPFCDLFTHDEWIDYQLQSLG 300
Db 241 ORLENDLSGVTLTDEVTYILMDMCSFDTISTSTVDTKLSFPCDLFTHDEWINDYQLQSLN 300
QY 301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVODHTSTNHTLDSNPAIFPLNATLYADFS 360
Db 301 KYYGAGNPLGPTQGVGYANELLARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360
QY 361 HDNTMVSIFPAGLNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMOCEAKEP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSASWTVPFASRLYVEMMOCEAQEP 420
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QY 421 LVRVLVNDRVVPLHGGGVKLGCRKRDDEVEGLSFARSGGNWEECFA 467
Db 421 LVRVLVNDRVVPLHGGCPVDALGRCRTDSEFVKGLSFARSGGDWGECEFA 467

RESULT 15

US-10-083-452-11
; Sequence 11, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus ficuum
US-10-083-452-11

Query Match 74.4%; Score 1836; DB 14; Length 467;
Best Local Similarity 73.9%; Pred. No. 2.9e-176;
Matches 345; Conservative 42; Mismatches 80; Indels 3; Gaps 0;
QY 1 MGVEVWLLSTATLFGSTSTALGPRGNHSCDVTGGYQCFPEISHLMGTYSPPFSLADE 60
Db 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSCDVTGGYQCFSETSHLMGQYAPFSLANE 60
QY 61 SATSPDVPKGRVTFVQVLSRHGARYPTSSASKAYSALIEAQKNATAFKGYAFKTYN 120
Db 61 SVISPEVPACRVTFPAQVLSRHGARYPTDSKGYKYSALIEEQNATTFDKGYAFKTYN 120
QY 121 YTLGADDLTPFGQGMVNSGKIFRYKALARKIVPFIASGSDRVIASAEKFIQFOSA 180
Db 121 YSLGADDLTPFGQELVNSGKIFRYQYESTRNIVPFIASGSDRVIASAEKFIQFQST 180
QY 181 KLADPGANPHOASPVNVLIPGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPEIR 240
Db 181 KLADPRAQPCQSPKIDVVISSESSNNTLDPGCTVFEDELADTVFANFTATVPFSIR 240
QY 241 ARLEAHLPGVLTDEVDVNLMDMCPDVTARTQSLSPFCDLTHDEWIQYDYLSLG 300
Db 241 ORLENDLSGVTLTDEVIVLMDMCSPTTSTSTVDTKLSFFCDLTHDEWINYDYLSLK 300
QY 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db 301 KYGHGAGNPLGPTQGVYANELIARLTHSPVHDDTSSNHTLDSNPATFPLKSTLYADFS 360
QY 361 HONTMVSIFFALGLYNGTKPLSTTSVESIEETDGYASWTVFAARAYVEMMQCEAKEP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGESSAWTVFAASRLYVENMQCEAQAP 420
QY 421 LVRVLVNDRVVPLHGGGVKLGCRKRDDEVEGLSFARSGGNWEECFA 467
Db 421 LVRVLVNDRVVPLHGGCPVDALGRCRTDSEFVKGLSFARSGGDWAECEFA 467

Search completed: October 3, 2003, 08:12:32
Job time : 108.714 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:45 ; Search time 12.9581 Seconds
(without alignments)
1524.850 Million cell updates/sec

Title: US-09-488-265B-31

Perfect score: 2468
Sequence: 1 MGFFVLLSLATLFGSTG.....DFVEGLSFARSGGNWEECPA 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2308	93.5	467	US-09-273-871A-9	Sequence 9, Appli
2	2182	88.4	441	US-09-121-425-1	Sequence 1, Appli
3	2162	88.4	441	US-09-634-493A-1	Sequence 1, Appli
4	2170	87.9	467	US-09-121-425-2	Sequence 2, Appli
5	2170	87.9	467	US-09-634-493A-2	Sequence 2, Appli
6	1888	76.5	465	US-08-868-435-33	Sequence 33, Appli
7	1888	76.5	465	US-08-744-231-33	Sequence 33, Appli
8	1888	76.5	465	US-09-044-718-78	Sequence 78, Appli
9	1888	76.5	465	US-09-636-499-6	Sequence 8, Appli
10	1888	76.5	465	US-09-273-871A-8	Sequence 8, Appli
11	1880	76.2	465	US-09-044-718-80	Sequence 80, Appli
12	1879	76.1	465	US-09-044-718-79	Sequence 79, Appli
13	1878	76.1	439	US-09-044-718-3	Sequence 3, Appli
14	1878.5	76.1	449	US-09-044-718-12	Sequence 12, Appli
15	1876	76.0	465	US-09-044-718-81	Sequence 81, Appli
16	1854	75.1	469	US-09-044-718-82	Sequence 82, Appli
17	1852	75.0	467	US-07-923-724-8	Sequence 8, Appli
18	1852	75.0	467	US-08-609-426A-8	Sequence 8, Appli
19	1852	75.0	467	US-08-374-652C-2	Sequence 2, Appli
20	1848	74.9	467	US-08-151-574-32	Sequence 32, Appli
21	1848	74.9	467	US-08-146-424-20	Sequence 20, Appli
22	1848	74.9	467	US-08-693-709-2	Sequence 2, Appli
23	1848	74.9	467	US-08-419-448-32	Sequence 32, Appli
24	1848	74.9	467	US-08-819-825-3	Sequence 3, Appli
25	1848	74.9	467	US-09-163-642-3	Sequence 3, Appli
26	1848	74.9	467	US-09-233-510-32	Sequence 32, Appli
27	1848	74.9	467	US-09-636-499-5	Sequence 5, Appli

28	1841	74.6	467	3	US-09-155-855-3	Sequence 3, Appli
29	1841	74.6	467	4	US-09-543-744-3	Sequence 3, Appli
30	1841	74.6	467	4	US-09-929-060-3	Sequence 3, Appli
31	1836	74.4	467	4	US-09-273-871A-11	Sequence 11, Appli
32	1829	74.1	462	4	US-09-636-499-12	Sequence 12, Appli
33	1822	73.8	466	3	US-08-868-435-35	Sequence 35, Appli
34	1822	73.8	466	4	US-08-744-231-35	Sequence 35, Appli
35	1819	73.7	466	3	US-08-868-435-12	Sequence 12, Appli
36	1819	73.7	466	4	US-08-744-231-12	Sequence 12, Appli
37	1806	73.2	444	4	US-09-044-718-1	Sequence 1, Appli
38	1804.5	73.1	463	3	US-08-868-435-29	Sequence 29, Appli
39	1804.5	73.1	463	4	US-08-744-231-29	Sequence 29, Appli
40	1804.5	73.1	463	4	US-09-155-855-1	Sequence 10, Appli
41	1799	72.9	443	3	US-09-543-744-1	Sequence 1, Appli
42	1799	72.9	443	4	US-09-929-060-1	Sequence 1, Appli
43	1799	72.9	443	4	US-09-929-060-1	Sequence 1, Appli
44	1794	72.7	443	3	US-09-155-855-2	Sequence 2, Appli
45	1794	72.7	443	4	US-09-543-744-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-273-871A-9

Sequence 9, Application US/09273871A

Patent No. 6514495

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

TITLE OF INVENTION: Phytase Variants

FILE REFERENCE: 5618.500-US

CURRENT APPLICATION NUMBER: US/09/273, 871A

CURRENT FILING DATE: 1999-03-22

PRIOR APPLICATION NUMBER: PA 1998 00407

PRIOR FILING DATE: 1998-03-23

PRIOR APPLICATION NUMBER: PA 1998 00806

PRIOR FILING DATE: 1998-06-19

PRIOR APPLICATION NUMBER: PA 1998 01176

PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: PA 1999 00091

PRIOR FILING DATE: 1999-01-22

PRIOR APPLICATION NUMBER: 60/080,129

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/090,675

PRIOR FILING DATE: 1998-06-25

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 467

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Variation

US-09-273-871A-9

Query Match	93.5%	Score 2308;	DB 4;	Length 467;
Host local Similarity	93.4%	Pred. No. 1.2e-229;		
Matches 436;	Conservative 11;	Mismatches 20;	Indels 0;	Gaps 0;
Qy	1	MGFFVLLSLATLFGSTGTCALGPRGNHSCDTVDGGYOCFFPEISHLWGTYSPPFSLADE	60	
Dd	1	MGFFVLLSLATLFGSTGTCALGPRGNHSCDTVDGGYOCFFPEISHLWGTYSPPFSLADE	60	
Qy	61	SATSPDVPKGRVTFVQVLSRHGARYPTSSASKAYSALIEAOKNATAFKGYAEFLKTYN	120	
Dd	61	SATSPDVPDCCRTFVQVLSRHGARYPTSSASKAYSALIEAOKNATAFKGYAEFLKTYN	120	
Cy	121	YTLGADDLTPFGQQMVNSGKIFRYRYKALARKIVPFIASGSDRVIASAEKFIQFQSA	180	
Dd	121	YTLGADDLTPFGQMVNSGKIFRYRYKALARKIVPFIASGSDRVIASAEKFIQFQSA	180	
Qy	181	KLADPGANPHQSPVNIWILPEGAGYNTLDHGLCTAFEESELGDDVEANTAVFAPIR	240	

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Db 181 KLADPGSOPHCASPVIDVILPEGSYNNLTLDHGTCTAFEDSELGDDVEANFTALFAPATK 240
Qy 241 ARLEAHLPGVNLTDDEOVNLMDCPDTIVARTSDATQLSPFCDLFTDHEWIDYDLSLG 300
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Db 241 ARLEADLPVTLTDEDVYLMDMCPETIVARTSDATLSLSPFCALFTDHEWROYDYLSLG 300
Qy 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVDHTSTNHTLDSNPATPLNATLYADPS 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVDHTSTNHTLDSNPATPLNATLYADPS 360
Qy 361 HDNPMWIFFALGLYNGTKPLSTTSVESIETDGYASMTVPFAARAYVEMMOCEAREP 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 HDNSMISIFALGLYNGTAPLSTTSVESIETDGYASMTVPFGARAYVEMMOCEAREP 420
Qy 421 LVRVLVNDVRVPLHGCGVDKGRCKRDDFVEGLSFARSGGNWEECPA 467
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Db 421 LVRVLVNDVRVPLHGCAVDKGRCKRDDFVEGLSFARSGGNWEECPA 467

RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; PRIOR FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-121-425-1
Query Match 88.4%; Score 2182; DB 3; Length 441;
Best Local Similarity 93.0%; Pred. No. 1.le-216;
Matches 410; Conservative 11; Mismatches 20; Indels 0; Gaps 0;
Qy 27 NSHSCDIVDGGYQCFPEISHLWGTSPFFSLADESALSIPDKGCRVTFVQVLSRHGARY 86
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Db 1 NSHSCDIVDGGYQCFPEISHLWGTSPFFSLEDESALSIPDPDCKRTFVQVLSRHGARY 60
Qy 87 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNLTIGADDLTFFGEOQMVNSGKIFERR 146
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Db 61 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNLTIGADDLTFFGEOQMVNSGKIFERR 120
Qy 147 YKALARKIVPIRAGSDRVIASAEKIEGFSQAKLADPGANPHQASPVINVIPEGAGY 206
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Db 121 YKALARKIVPIRAGSDRVIASAEKIEGFSQAKLADPGSQPHQASPVIDVIPEGAGY 180
Qy 207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPTRARLEAHLPGVNLTDDEVNLMDCPFF 266
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Db 181 NNTLDHGLCTAFEESELGDDVEANFTALFAPARLEADLPVTLTDEDVYVLMDCPFF 240
Qy 267 DTVARTSDATLSLSPFCDLFTDHEWIDYDLSLGKYYGYGAGNPLGPAQGVFNELIAR 326
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 ETVARTSDATLSLSPFCALFTDHEWROYDYDLSLGKYYGYGAGNPLGPAQGVGFANELIAR 300
Qy 327 LTHSPVDHTSTNHTLDSNPATPLNATLYADFSHDNTMYSIFFALGLYNGTKPLSTTSV 386
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 LTRSPVDHTSTNHTLDSNPATPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360
Qy 387 ESIEETDGYASMTVPFAARAYVEMMOCEAREKPELVRVLVNDVRVPLHGCGVDKGRCKR 446
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Db 361 ESIEETDGYASMTVPFGARAYVEMMOCEAREKPELVRVLVNDVRVPLHGCAVDKGRCKR 420
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Qy 447 DDFVEGLSFARSGGNWEECPA 467
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Db 421 DDFVEGLSFARSGGNWEECPA 441

RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634.493A
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121.425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-634-493A-1
Query Match 88.4%; Score 2182; DB 4; Length 441;
Best Local Similarity 93.0%; Pred. No. 1.le-216;
Matches 410; Conservative 11; Mismatches 20; Indels 0; Gaps 0;
Qy 27 NSHSCDIVDGGYQCFPEISHLWGTSPFFSLADESALSIPDKGCRVTFVQVLSRHGARY 86
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Db 1 NSHSCDIVDGGYQCFPEISHLWGTSPFFSLEDESALSIPDPDCKRTFVQVLSRHGARY 60
Qy 87 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNLTIGADDLTFFGEOQMVNSGKIFERR 146
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Db 61 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNLTIGADDLTFFGEOQMVNSGKIFERR 120
Qy 147 YKALARKIVPIRAGSDRVIASAEKIEGFSQAKLADPGANPHQASPVINVIPEGAGY 206
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 YKALARKIVPIRAGSDRVIASAEKIEGFSQAKLADPGSQPHQASPVIDVIPEGAGY 180
Qy 207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPTRARLEAHLPGVNLTDDEVNLMDCPFF 266
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Db 181 NNTLDHGLCTAFEESELGDDVEANFTALFAPARLEADLPVTLTDEDVYVLMDCPFF 240
Qy 267 DTVARTSDATLSLSPFCDLFTDHEWIDYDLSLGKYYGYGAGNPLGPAQGVFNELIAR 326
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Db 241 ETVARTSDATLSLSPFCALFTDHEWROYDYDLSLGKYYGYGAGNPLGPAQGVGFANELIAR 300
Qy 327 LTHSPVDHTSTNHTLDSNPATPLNATLYADFSHDNTMYSIFFALGLYNGTKPLSTTSV 386
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Db 301 LTRSPVDHTSTNHTLDSNPATPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360
Qy 387 ESIEETDGYASMTVPFAARAYVEMMOCEAREKPELVRVLVNDVRVPLHGCGVDKGRCKR 446
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Db 361 ESIEETDGYASMTVPFGARAYVEMMOCEAREKPELVRVLVNDVRVPLHGCAVDKGRCKR 420
Qy 447 DDFVEGLSFARSGGNWEECPA 467
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Db 421 DDFVEGLSFARSGGNWEECPA 441
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RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
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; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-121-425-2

Query Match      87.9%; Score 2170; DB 3; Length 467;
Best Local Similarity 85.4%; Pred. No. 2.2e-215;
Matches 416; Conservative 11; Mismatches 20; Indels 40; Gaps 2;

QY 1 MGCVFVLLSLATLFGSTSGTALGPRGNHSCDVTGQYQCFPEISHLWCTYSPFFSLADE 60
DB 1 MGCVFVLLSLATLFGSTSGTALGPRGNHSCDVTGQYQCFPEISHLWCTYSPFFSLADE 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFKTYN 120
DB 61 SAISPDVPDCCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFKTYN 120
QY 121 YTLGADDLTPGEOOMVNSGKIFRYRYKALARKIVPPFIRASGSDRVIASAEKIEGFOSA 180
DB 101 YTLGADDLTPGEOOMVNSGKIFRYRYKALARKIVPPFIRASGSDRVIASAEKIEGFOSA 160
QY 181 KLADPGANPHQASPVIN-----VIIPEGAGYNNTLDHGLCTAFEE 220
DB 161 KLADPGSQPHQASPVIDLIEAIOKNATAFKGYAFKLVIIPEGAGYNNTLDHGLCTAFED 220
QY 221 SELGDDVEANTAVFAPPIRLEAHLPGVNLTDVVDVNMDCPFDVTARTSDATQLSP 280
DB 221 SELGDDVEANTAVFAPPIRLEAHLPGVNLTDVVDVNMDCPFDVTARTSDATQLSP 280
QY 281 FCDLTHDEWQYDYLOSGLKYYGYGAGNPLGPAQGYGVFNELIARLTHSPVODHTSTNH 340
DB 281 FCALETHDEWQYDYLOSGLKYYGYGAGNPLGPAQGYGVFNELIARLTHSPVODHTSTNH 340
QY 341 TLDSNPATFPLNATLYADFSDHNTWVSIFFALGLYNGTKPLSTSVESIEETOGYSASWT 400
DB 341 TLDSNPATFPLNATLYADFSDHNTWVSIFFALGLYNGTKPLSTSVESIEETOGYSASWT 400
QY 401 VPFARAYVENMQCAEKEPLRVLVNDRVVPLHGCAGVDKLGCRKRDVFEGLSFARSGG 460
DB 401 VPFARAYVENMQCAEKEPLRVLVNDRVVPLHGCAGVDKLGCRKRDVFEGLSFARSGG 460
QY 461 NWEECEFA 467
DB 461 NWAECFA 467
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RESULT 5

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US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634.493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121.425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-634-493A-2
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Query Match 87.9%; Score 2170; DB 4; Length 467;

Best Local Similarity 85.4%; Pred. No. 2.2e-215;

Matches 416; Conservative 11; Mismatches 20; Indels 40; Gaps 2;

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QY 1 MGCVFVLLSLATLFGSTSGTALGPRGNHSCDVTGQYQCFPEISHLWCTYSPFFSLADE 60
DB 1 MGCVFVLLSLATLFGSTSGTALGPRGNHSCDVTGQYQCFPEISHLWCTYSPFFSLADE 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFKTYN 120
DB 61 SAISPDVPDCCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFKTYN 120
QY 121 YTLGADDLTPGEOOMVNSGKIFRYRYKALARKIVPPFIRASGSDRVIASAEKIEGFOSA 180
DB 101 YTLGADDLTPGEOOMVNSGKIFRYRYKALARKIVPPFIRASGSDRVIASAEKIEGFOSA 160
QY 181 KLADPGANPHQASPVIN-----VIIPEGAGYNNTLDHGLCTAFEE 220
DB 161 KLADPGSQPHQASPVIDLIEAIOKNATAFKGYAFKLVIIPEGAGYNNTLDHGLCTAFED 220
QY 221 SELGDDVEANTAVFAPPIRLEAHLPGVNLTDVVDVNMDCPFDVTARTSDATQLSP 280
DB 221 SELGDDVEANTAVFAPPIRLEAHLPGVNLTDVVDVNMDCPFDVTARTSDATQLSP 280
QY 281 FCDLTHDEWQYDYLOSGLKYYGYGAGNPLGPAQGYGVFNELIARLTHSPVODHTSTNH 340
DB 281 FCALETHDEWQYDYLOSGLKYYGYGAGNPLGPAQGYGVFNELIARLTHSPVODHTSTNH 340
QY 341 TLDSNPATFPLNATLYADFSDHNTWVSIFFALGLYNGTKPLSTSVESIEETOGYSASWT 400
DB 341 TLDSNPATFPLNATLYADFSDHNTWVSIFFALGLYNGTKPLSTSVESIEETOGYSASWT 400
QY 401 VPFARAYVENMQCAEKEPLRVLVNDRVVPLHGCAGVDKLGCRKRDVFEGLSFARSGG 460
DB 401 VPFARAYVENMQCAEKEPLRVLVNDRVVPLHGCAGVDKLGCRKRDVFEGLSFARSGG 460
QY 461 NWEECEFA 467
DB 461 NWAECFA 467
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RESULT 6

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US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-744-231-33

Query Match 76.5%: Score 1888; DB 4; Length 465;
Best Local Similarity 76.9%: Pred. No. 2.9e-186;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGTALGPRGNSHSCDVTGGYQCQCFEISHLWGTSPPFSLADE 60
DB 1 MYTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQYSPFFSLEDE 59
QY 61 SAISPDPVKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKYAFKLYN 120
DB LSVSSKLPKDCRITLVQVLSRHGARYPTSSASKYKLVTAIOANATDFKGFALFKN 119
QY 121 YTLGADDLTPFGEQOMVNSGKIFYRRYKALARKIVPFIRASGSDRVIASAEKFIQFQSA 180
DB YTLGADDLTPFGEQOLVNSGKIFYQRYKALARSVPFIRASGSDRVIASGEKFIQFQQA 179
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
DB KLADPGAT-NRAAPALSVIIEPESETFNNTLDHGVCCTKFEASQLGDEVAANFTALFAPDIR 238
QY 241 ARLEAHLPGVNLTDDEVDVNLMDKCPFDIVARTSDAIOQLSPFCDLFTHDEWYQYDYLQSLG 300
DB ARAEKHLPGVTLTDDEVDVSLMDKCFDIVARTSDASQISPCQLFTHNEWKKNYLOSLG 298
QY 301 KYCYGAGNPLGPAQGVGNELIARLTHSPVODHTSTNHTLDSNPATFFPLNATHYVDFS 360
DB KYCYGAGNPLGPAQGVGNELIARLTHSPVODHTSTNHTLDSNPATFFPLNATHYVDFS 358
QY 361 HDNTWYSIFFALGLYNGTKPLSTTSVESIEETDGYSSASVTVPFAARAYVEMMOCEAKEP 420
DB HDNSWVSIFFALGLYNGTEPLSRTSVESAKELDGYSSASVVPFGARAYFETMOCKSEKEP 418
QY 421 LVRVLVNDRVVPLHGGVDKLGRCRDRDFVEGLSFARSGNWECEFA 467
DB LVRALINDRVVPLHGGVDKLGRCRLNDFVKGLSWARSGGNWGECEFS 465

RESULT 8
US-09-044-718-78
Sequence 78, Application US/09044718
Patent No. 6391605
GENERAL INFORMATION:
APPLICANT: KOSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: van LOON, Adolphus
APPLICANT: VOGEL, Kurt
APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 78
LENGTH: 465
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-09-044-718-78

Query Match 76.5%: Score 1888; DB 4; Length 465;
Best Local Similarity 76.9%: Pred. No. 2.9e-186;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGTALGPRGNSHSCDVTGGYQCQCFEISHLWGTSPPFSLADE 60
DB 1 MYTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQYSPFFSLEDE 59

QY 61 SAISPDPVKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKYAFKLYN 120
DB LSVSSKLPKDCRITLVQVLSRHGARYPTSSASKYKLVTAIOANATDFKGFALFKN 119
QY 121 YTLGADDLTPFGEQOMVNSGKIFYRRYKALARKIVPFIRASGSDRVIASAEKFIQFQSA 180
DB YTLGADDLTPFGEQOLVNSGKIFYQRYKALARSVPFIRASGSDRVIASGEKFIQFQQA 179
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
DB KLADPGAT-NRAAPALSVIIEPESETFNNTLDHGVCCTKFEASQLGDEVAANFTALFAPDIR 238
QY 241 ARLEAHLPGVNLTDDEVDVNLMDKCPFDIVARTSDAIOQLSPFCDLFTHDEWYQYDYLQSLG 300
DB ARAEKHLPGVTLTDDEVDVSLMDKCFDIVARTSDASQISPCQLFTHNEWKKNYLOSLG 298
QY 301 KYCYGAGNPLGPAQGVGNELIARLTHSPVODHTSTNHTLDSNPATFFPLNATHYVDFS 360
DB KYCYGAGNPLGPAQGVGNELIARLTHSPVODHTSTNHTLDSNPATFFPLNATHYVDFS 358
QY 361 HDNTWYSIFFALGLYNGTKPLSTTSVESIEETDGYSSASVTVPFAARAYVEMMOCEAKEP 420
DB HDNSWVSIFFALGLYNGTEPLSRTSVESAKELDGYSSASVVPFGARAYFETMOCKSEKEP 418
QY 421 LVRVLVNDRVVPLHGGVDKLGRCRDRDFVEGLSFARSGNWECEFA 467
DB LVRALINDRVVPLHGGVDKLGRCRLNDFVKGLSWARSGGNWGECEFS 465

RESULT 9
US-09-636-499-6
Sequence 6, Application US/09636499
Patent No. 6475762
GENERAL INFORMATION:
APPLICANT: Stafford, Christian F.
APPLICANT: Trinci, Anthony P.J.
APPLICANT: Brookman, Jayne L.
TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Sam
FILE REFERENCE: GC586-2
CURRENT APPLICATION NUMBER: US/09/636,499
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/148,960
PRIOR FILING DATE: 1999-06-13
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 465
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-09-636-499-6

Query Match 76.5%: Score 1888; DB 4; Length 465;
Best Local Similarity 76.9%: Pred. No. 2.9e-186;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGTALGPRGNSHSCDVTGGYQCQCFEISHLWGTSPPFSLADE 60
DB 1 MYTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQYSPFFSLEDE 59
QY 61 SAISPDPVKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKYAFKLYN 120
DB LSVSSKLPKDCRITLVQVLSRHGARYPTSSASKYKLVTAIOANATDFKGFALFKN 119
QY 121 YTLGADDLTPFGEQOMVNSGKIFYRRYKALARKIVPFIRASGSDRVIASAEKFIQFQSA 180
DB YTLGADDLTPFGEQOLVNSGKIFYQRYKALARSVPFIRASGSDRVIASGEKFIQFQQA 179
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
DB KLADPGAT-NRAAPALSVIIEPESETFNNTLDHGVCCTKFEASQLGDEVAANFTALFAPDIR 238

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Qy 241 ARLEAHLPGVNLTDDEVVNLMDMCPFTVARTSATQSLSPFCULFTHDDEWIOYDIQSLG 300
Db 239 ARAEKHLPGVTLTDEDEVVSLMDMGSFDTVARTSDASQLSPFCULFTHDDEWKKYNYLQSLG 258
Qy 301 KYYGAGNPLGPGAGVGFVNELIARLTGHSVPQDHTSTNHTLDSNPATPLNAILYADFS 360
Db 299 KYYGAGNPLGPGAGIGFTNELLARLTGSPVQDHTSTNTLSNPATPLNATWYVDFS 358
Qy 361 HDNTMYSIFFALGLYNGTKPLSTISVSIESIETDGYASMTVPFAARAYVNMOCFAKEP 420
Db 359 HONSMYSIFFALGLYNGTEPLSRTSVESAKELDGYASWVVPFGARAYETMOCKSEKEP 418
Qy 421 LVRLVLYNDRVPLRHCGGVDKLGRCKRDFVEGLSFBSSGNNWEECEFA 467
Db 419 LVRLALINDRVPLRHGCDVKLGRCKLNDVFKGUSWARSNGNWECEFS 465

RESULT 10
US-09-773-871A-8
: Sequence 8, Application US/09273871A
: Patent No. 6514495
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618.500-US
: CURRENT APPLICATION NUMBER: US/09/273.871A
: CURRENT FILING DATE: 1998-03-22
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-09-19
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: PRIOR FILING DATE: 1998-06-25
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 465
: TYPE: PRF
: ORGANISM: Aspergillus fumigatus
US-09-773-871A-8

Query Match 76.5%; Score 1888; DB 4; Length 465;
Best Local Similarity 76.9%; Pred No. 2.9e-186;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2

Qy 1 MGVVVVLLSIATLPFGSTGATLPGRGNHSCDTVDGGYQCGFPELSHLWGYSPPFSLAJE 60
Db 1 MVTLTPLTAAAYLLSGRVSAAAPSSAG-SKSCDTVDLGVQCGSPATSHLWGYSPPFSLDE 59
Qy 61 SAISPDVPGKGVIFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAPKGYAFILKTYN 120
Db 60 LSVSSKIPKOCRTILVQVLSRHGARYPTSSKKYKKLVTAIQNATDFGKGFAPLKTIN 119
Qy 121 YTLGADDLTPFGEQQMVNSGIKFYBRYKALARKIVPFIIRASGSDRVIASAEKEIEGFQA 180
Db 120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVPFIIRASGSDRVIASCEKFIEGFOQA 179
Qy 181 KLADPGANPHQASPVINVIIPGAGYNNLTDLHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 180 KLADPGAT-NRAAPAIISVPIPESEIFNNLTDLHGVTCTFEASQLGDEVAANFTALFAPDIR 238
Qy 241 ARLEAHLPGVNLTDDEVVNLMDMCPFDVARTSATQSLSPFCULFTHDDEWIOYDIQSLG 300
Db 239 ARAEKHLPGVTLTDEDEVVSLMDMGSFDTVARTSDASQLSPFCULFTHDDEWKKYNYLQSLG 298
Qy 301 KYYGAGNPLGPGAGVGFVNELIARLTGHSVPQDHTSTNHTLDSNPATPLNAILYADFS 360

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RESULT 12

US-09-044-718-79
: Sequence 79, Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 79
: LENGTH: 465
: TYPE: PRI
: ORGANISM: Aspergillus fumigatus
US-09-044-718-79

Query Match 76.1% Score 1879; DB 4; Length 465;
Best Local Similarity 76.7% Pred. No. 2.5e-185;
Matches 358; Conservative 35; Mismatches 72; Indels 2; Gaps 2;
QY 1 MGVVVLLSIATLFGSTGTALGPRNSHSCDVTGQYQCFPEISHLWGTSPFFSLADE 60
Db 1 MVTLTLLSAAYLLSGRVSASPAG-SKSCDIVDLGQSPATSHLWGOYSPFFSLADE 59
QY 61 SAISPDVPGRCRTVFQVLSRHGARYPTSSAKAYSALIEAQKNATAKGYAFKLTYN 120
Db 60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKKYKLVTAIQANATDFKGFALKTYN 119
QY 121 YTLGADDLTPFGQOQMVNSGIKRYRYKALARKIVPFIASGSDRVIASAEKFIQFQSA 180
Db 120 YTLGADDLTPFGQOQMVNSGIKRYRYKALARKIVPFIASGSDRVIASAEKFIQFQSA 179
QY 181 KADPGANPHQASPVINVIPEGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPP 240
Db 180 KADPGAT-NRAAPAISSVIIPESETFTNNTLDHGVCTKFEASQLGDEVAANFTALEAPDIR 238
QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPDVTVAKTSDATQLSPFCGLFTHDEWIQYDYLQSLG 300
Db 239 AREKHLPGVNLTDDEVVNLMDMCSFTVARTSDASQLSPFCGLFTHDEWIQYDYLQSLG 298
QY 301 KYGYGAGNPLGPAQGVGFVNEILARLTHSPVQDHTSTNHTLDSNPATFPLNATLYAFDS 360
Db 299 KYGYGAGNPLGPAQGGIGFTNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYAFDS 358
QY 361 HDNTWVSIFPAGLYNGIKPLSTTSVESIEETDGYASWTVPFAARAYVENMOCEAEKEP 420
Db 359 HDNSWVSIFPAGLYNGTEGLSTSVESAEKELDGYASWVVPFGARAYFETWOCKSEKEP 418
QY 421 LVRVLVNDRVVPLHGGVDKLGRCRCKDDFVEGLSFARSGGNWCECFA 467
Db 419 LVRALINDRVVPLHGGVDKLGRCCKLNDLVKGLSWARSGGNWCECFS 465

RESULT 13

US-09-044-718-3
: Sequence 3, Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus

: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 439
: TYPE: PRI
: ORGANISM: Aspergillus fumigatus
US-09-044-718-3

Query Match 76.1% Score 1878.5; DB 4; Length 439;
Best Local Similarity 79.8% Pred. No. 2.6e-185;
Matches 351; Conservative 35; Mismatches 53; Indels 1; Gaps 1;
QY 28 SHSCDVTGQYQCFPEISHLWGTSPFFSLADESAISPDVPGRCRTVFQVLSRHGARYP 87
Db 1 SKSCDVTGQYQCFPEISHLWGTSPFFSLADELSVSKLPKDCRITLVQVLSRHGARYP 60
QY 88 TSSAKAYSALIEAQKNATAKGYAFKLTYNLTGADDLTPFGQOQMVNSGIKRYRY 147
Db 61 TSSKSKYKLVTAIQANATDFKGFALKTYNLTGADDLTPFGQOQMVNSGIKRYRY 120
QY 148 KALARKIVPFIASGSDRVIASAEKFIQFQSAKADPGANPHQASPVINVIPEGAGYN 207
Db 121 KALARSVPFIASGSDRVIASAEKFIQFQSAKADPGAT-NRAAPAISSVIIPESETFN 179
QY 208 NTLDHGLCTAFEESELGDDVEANFTAVFAPPFIRARLEAHLPGVNLTDDEVVNLMDMCPD 267
Db 180 NTLDHGVCTKFEASQLGDEVAANFTALPAPDIRARAEKHLPGVTLTDDEVVNLMDMCSFD 239
QY 268 TVARTSDAQLSPFCGLFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFVNEILARL 327
Db 240 TVARTSDASQLSPFCGLFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGGIGFTNELIARL 299
QY 328 THSPVQDHTSTNHTLDSNPATFPLNATLYAFDSHDNTWVSIFPAGLYNGTEPLSTTSVE 387
Db 300 TRSPVQDHTSTNHTLDSNPATFPLNATLYAFDSHDNSWVSIFPAGLYNGTEPLSTTSVE 359
QY 388 SIETDGYASWTVPFAARAYVENMOCEAEKEP LVRVLVNDRVVPLHGGVDKLGRCRCK 447
Db 360 SAKELDGYASWVVPFGARAYFETWOCKSEKEPLVRALINDRVVPLHGGVDKLGRCCKLN 419
QY 448 DFVEGLSFARSGGNWCECFA 467
Db 420 DFVKGLSWARSGGNWCECFS 439

RESULT 14

US-09-044-718-12
: Sequence 12, Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 12
: LENGTH: 449
: TYPE: PRI

ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Query Match 76.1%; Score 1878.5; DB 4; Length 449;
Best Local Similarity 79.8%; Pred. No. 2.6e-185;
Matches 351; Conservative 35; Mismatches 53; Indels 2; Gaps 2;

Qy 28 SHSCOTVDGCGCFEISHLWGTYSPPFSLADESAISPDVPGKGRVTVQVLSRHGARYP 87
Db 11 SKSCDTVDLGYCSPATSHLWQYSPFFSLEDELVSXKLPKCRITLVQVLSRHGARYP 70

Qy 88 TSASAKAYSALTEAKGNATAPKGYAFUKTYNYTLGADDLTPGCEQOMVNSGKFYRRY 147
Db 71 TSSKSKYKLLTAQANATDFKFAFLKTYNYTLGADDLTPGCEQOLVNSGKFKYQY 130

Qy 148 KALARKIVFFIRASGSDRVIAAEKPIEGFQSAKIALDPGANPHQASPVNVIPEGAGYN 207
Db 131 KALARSVWPFIRASGSDRVIAASGEKPIEGFQOAKLADPGAT-NRAAPAIISVIIPESETFN 189

Qy 208 NTLDHGLCTAFSESELGDDVEANFTAVFAPTRARLEAHLPCVNLTDSDVNLMDMCPD 267
Db 190 NTLDHGCVTKFASQGLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSJMDMCSFD 249

Qy 268 TVARTSDATQSPFCDLTHDWMQYDYLQSLGKYGYGAGNPLGPAQGVGVNLIARL 327
Db 250 TVARTSDASQSPFCOLFTHNEWKYNYLQSLGKYGYGAGNPLGPAQGVGVNLIARL 309

Qy 328 THSPVDHTSTNHTLDSNPATPLNATLYADFSHONTWYSIFFALGLYNGTKPIST-SVE 387
Db 310 THSPVDHTSTNHTLDSNPATPLNATLYADFSHONTWYSIFFALGLYNGTKPIST-SVE 369

Qy 388 SIBEIDGYSASMTVPFAARAYVEMMOCEAEKEPLVRLVNDRVVPLHGGCVDKLGRCKRD 447
Db 370 SAKELDGYASWVVPFGARAYFETMOCKSEKEPLVRLVNDRVVPLHGGCVDKLGRCKLN 429

Qy 448 DFVEGLSFARSGGNWEECEFA 467
Db 430 DFVKGLSWARSGGNWGECEFS 449

RESULT 15
US-09-044-718-81
; Sequence 81. Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-81

Query Match 76.0%; Score 1876; DB 4; Length 465;
Best Local Similarity 76.4%; Pred. No. 5.1e-185;
Matches 357; Conservative 36; Mismatches 72; Indels 2; Gaps 2;

Qy 1 MGVEFWLLSLATLFGSTSGTALGPRGNHSCDVTGCGYOCFPEISHLWGTYSPPFSLADE 60
Db 1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWQYSPFFSLEDE 59

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-XGAPEXT=7 -YGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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1	2308	92.5	467	14	US-10-083-452-9	Sequence 9, Appl.
2	1888	75.9	465	14	US-10-083-452-8	Sequence 8, Appl.
3	1888	75.9	465	15	US-10-062-848-78	Sequence 78, Appl.
4	1888	75.9	465	15	US-10-229-358-6	Sequence 6, Appl.
5	1881.5	75.7	474	15	US-10-213-990-24	Sequence 24, Appl.
6	1880	75.6	465	15	US-10-062-848-80	Sequence 80, Appl.
7	1879	75.6	465	15	US-10-062-848-79	Sequence 79, Appl.
8	1878.5	75.6	439	15	US-10-062-848-3	Sequence 3, Appl.
9	1878.5	75.6	449	15	US-10-062-848-12	Sequence 12, Appl.
10	1876	75.5	465	15	US-10-062-848-81	Sequence 81, Appl.
11	1854	74.6	469	15	US-10-062-848-82	Sequence 82, Appl.
12	1848	74.3	467	15	US-10-075-709-32	Sequence 32, Appl.
13	1848	74.3	467	15	US-10-229-358-5	Sequence 5, Appl.
14	1841	74.1	467	9	US-09-929-060-3	Sequence 3, Appl.
15	1836	73.9	467	14	US-10-083-452-11	Sequence 11, Appl.
16	1829	73.6	462	15	US-10-229-358-12	Sequence 12, Appl.
17	1806	72.6	444	15	US-10-062-848-1	Sequence 1, Appl.
18	1804.5	72.6	463	14	US-10-083-452-20	Sequence 20, Appl.
19	1799	72.4	443	9	US-09-929-060-1	Sequence 1, Appl.
20	1794	72.0	443	9	US-09-929-060-2	Sequence 2, Appl.
21	1789.5	72.0	447	15	US-10-062-848-6	Sequence 6, Appl.
22	1752	70.5	466	14	US-10-083-452-12	Sequence 12, Appl.
23	1752	70.5	466	15	US-10-229-358-7	Sequence 7, Appl.
24	1748	70.3	450	15	US-10-062-848-15	Sequence 15, Appl.
25	1710	68.8	466	14	US-10-083-452-13	Sequence 13, Appl.
26	1706.5	68.6	450	15	US-10-062-848-9	Sequence 9, Appl.
27	1697	68.3	438	15	US-10-062-848-2	Sequence 2, Appl.
28	1658	66.7	489	15	US-10-229-358-4	Sequence 4, Appl.
29	1658	66.7	489	15	US-10-229-358-10	Sequence 10, Appl.
30	1623	65.3	410	15	US-10-229-358-11	Sequence 11, Appl.
31	1381	55.6	475	14	US-10-083-452-14	Sequence 14, Appl.
32	1339	53.9	355	15	US-10-229-358-15	Sequence 15, Appl.
33	1334.5	53.7	487	14	US-10-083-452-15	Sequence 15, Appl.
34	1334.5	53.7	487	15	US-10-229-358-8	Sequence 8, Appl.
35	1215	48.9	495	14	US-10-083-452-3	Sequence 3, Appl.
36	1210	48.7	478	14	US-10-083-452-3	Sequence 3, Appl.
37	920	37.0	284	15	US-10-229-358-19	Sequence 19, Appl.
38	867	34.9	283	15	US-10-229-358-9	Sequence 9, Appl.
39	867	34.9	283	15	US-10-229-358-24	Sequence 24, Appl.
40	845.5	34.0	443	14	US-10-083-452-5	Sequence 5, Appl.
41	833.5	33.5	453	14	US-10-083-452-6	Sequence 6, Appl.
42	830.5	33.4	439	14	US-10-083-452-7	Sequence 7, Appl.
43	825	33.2	442	14	US-10-083-452-4	Sequence 4, Appl.
44	729.5	29.3	212	15	US-10-229-358-16	Sequence 16, Appl.
45	406	16.3	312	15	US-10-229-358-21	Sequence 21, Appl.

ALIGNMENTS

RESULT 1
US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication: No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Ailan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273.871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25

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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation:
US-10-083-452-9

Alignment Scores:
Pred. No.:      2,79e-181      Length:      467
Score:          2308.00      Matches:      436
Percent Similarity: 95.72%      Conservative: 11
Best Local Similarity: 93.36%      Mismatches:   20
Query Match:      92.84%      Indels:       0
DB:              14          Gaps:         0

US-09-488-265B-30 (1-1404) x US-10-083-452-9 (1-467)

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Db 1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20
QY 61 GCCTTGGCTCTCCGTGTACICTCACTCTGTGACACTGTCACGCTGTTCACAAATGT 120
Db 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40
QY 121 TTCGCAGAAATTTCTCACTGTGTGGGTACATCTCTCCATCTCTCTTTGGCTGACCAA 180
Db 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
QY 181 TCTGCTATTCTCCAGACGCTCCAAAGGUTGTAGAGTTACTTTCGTTCCAAGCTTTGTC 240
Db 61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80
QY 241 AGACAGGTGTGTAGATACCCAACTCTTCTGCGTCTTAAGCGGTACTCTGCTTTGATGAA 300
Db 81 ArGHisGlyAlaArGty:ProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGAAGCTACTGCTTCAAGGTAAGTACGCTTCTTGAAAGACTTACAAAC 360
Db 101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACATTTGGGTGTGAGGACTTGACTCCANTCGGTGACACAAATGGTAACTCTGGT 420
Db 121 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140
QY 421 ATTAACCTTCTACAGAAGATACAAGCGCTTGGCTACAAGATGTTCCATTCATTAGAGCT 480
Db 141 IleLysPheTyrArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 160
QY 481 TCTGTTCTGCAGAGATTATTGCTTCTGCTGCAAAAGTTCATTCAAGAGTTCCAACTGCT 540
Db 161 SerGlySerAspArgValIleAlaSerAlaGlnLysPheIleGlyPheGlnSerAla 180
QY 541 AAGTTGGCTGACCCAGGTGTCAAACCCACCAAGCTTCTCCAGTTATTAACTGTTATTAT 600
Db 181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIleTle 200
QY 601 CCAGAAGGTGCTGGTTACAACAACACTTGGACACAGGTTTGCTACTGCTTCGAGNA 660
Db 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY 661 TCTGAATTGGGTGACGAGCTTGAAGCTAACTTCACTGCTGCTTTTTCGCTCCACCAATTGA 720
Db 221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
QY 721 GCTAGATTGGAAGCTCACTTCCCGAGGTGTAACTTGACTGACCAAGACAGCTGTGTTA 780
Db 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
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Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59
Qy 181 TCTGCTATTCTCCAGACCTCCAAAGGCTCTACAGTTACTTTCTGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
Qy 241 AGACAGCGTCTAGATACCCAACTTCTTCTCGCTCTAAGGGCTACTCTGCTTTGATTGAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLeuValThr 99
Qy 301 GCTATTCAAAGACGCTACTGCTTTCAGGGTAACTAGCTTTCTTGAAGCTTACAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
Qy 361 TACACTTTGGTGGTCTGACGACTTGCATCCATTCGGTGAACAAATGTTAACTCTGCT 420
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
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Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaLeuAlaArgSerValProPheIleArgAla 159
Qy 481 TCTGGTCTGACAGACTTATCTGCTGCTGAAAGTTCAITGAAGTTTCCAACTCTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
Qy 541 AAGTTGGTGCACCGCTGCTTAACCCACACAGCTTCTCCAGTTATTAACTATTATT 600
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Qy 601 CCAGAAGTCTGTTTACACAACTTTGGACCGGTTTGTGTGCTGCTTTCGAAGAA 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 216
Qy 661 TCTGAATTTGGTGCACGAGCTGAAGCTTAAGCTACCTGCTGCTGCTGCTGCTGCTGCT 720
Db 219 SerGlnLeuGlyAspGluAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
Qy 721 GCTAGATTGGAAGCTCACTTCCAGGTTTAACTTGACTGACGAAGAGCTTGTAACTTG 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
Qy 781 ATGACATGTGTCATTCGACACTGTGTGCTAGAACTTCTGACGCTACTCAATTTGCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaAlaArgThrSerAspAlaSerGlnLeuSerPro 278
Qy 841 TCTGCTGACTTGTCTACCTACGACGATGGATTCATACGACTACTTCCAACTTTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
Qy 901 AAGTACTACGGTTACGGTCTGCTGAACCCATTTGGGTCCAGCTCAAGGTTGTTTCTGTT 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
Qy 961 AACGAATTGATTGCTAGATTGACTACTCTCCAGTTTCAAGACACACTTCTACTAACCAC 1020
Db 319 AsnGlnLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
Qy 1021 ACTTGTGACTCTAACCCAGCTACTTCCCATTTGAACGCTTACTTTGTACCGCTGCTTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
Qy 1081 CAGCACAACTATGTTTCTTATTTCTTCGCTTTGGGTTTGTACAACGCTACTAAGGCA 1140
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Qy 1141 TGTCTACTTCTTCTGTAATCTATGAAGAACTGACGGTGTACTCTGCTTCTTGGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
Qy 1201 GTTCCATTGCTGCTAGAGCTTACGTTGAATGATGCAATGTGAAGCTGAAAGGACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
Qy 1261 TTGCTTAGAGTTTGTGTTAAACGACAGAGTTGTTCAATTCACAGGTTGTGTTCAAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
Qy 1321 TTGGGTAGATGTAAGAGACGACTTCGTTGAAGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
Qy 1381 AACTGGGAAGAATGTTTCGCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465

RESULT 4
US-10-229-358-6
; Sequence 6, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trincl, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-229-358-6

Alignment Scores:
Pred. No.: 9,97e-147 Length: 465
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 15 Gaps: 2

US-09-488-265b-30 (1-1404) x US-10-229-358-6 (1-465)
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Qy 61 GCCTGGTGGTCTCGTGAACCTCACTCTGTGACACTGTGTGACGGTGGTTACCAAGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
Qy 121 TTCCAGAAATTTCTCACTGTGGGGTACATCTCCATCTTCTCTTTTGGCTGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59
Qy 181 TCTGCTATTCTCCAGACCTCCAAAGGCTCTACAGTTACTTTCTGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
Qy 241 AGACAGCGTCTAGATACCCAACTTCTTCTCGCTCTAAGGGCTACTCTGCTTTGATTGAA 300
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Db 80 A-gHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLeuValThr 99
QY 301 GCTATTCAAAAGAGCGTACTGCTTTCAAGGGTAAGTACGGTTCCTTGAAGACATCAAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGTTGGTGAACAACAAATGGTTAACTCTGGT 420
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTTCTACAGAGATACAGGCTTGGCTAGAAAGATTGTTCATTTCATTAGAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TGTGGTCTGACAGAGATTATTGCTTCTGCTGAAAGTTCATTGAAGTTCCTCAATCTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
QY 541 AGTTGGCTGACCGAGTGTCAACCCACACCAAGCTTCTCCAGTTATTAAAGTATTAT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAAGGTGCTGTTACAAACACACTTTGGACACGCTTGTGACTGCTTTCGAAGAA 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TGTGAATGGTGACGACGCTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAAGCTCACCTGCGAGTGTAACTTGACTGACGAAGAGCTGTGTTAACTTG 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGACATGTGTCATTGACACACTGTGCTAGAACCTCTGACGCTACTCAATGTCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTTCTGACTGTTTCACTCAGCAGCAATGATTCATACGACTACTTGCATCTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGTTACGGTGTGTGTAACCATTTGGTCCAGCTCAAGGTGTGTTGTTTGGT 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AAGCAATTGATGCTAGATTGACTACTCTCCAGTTCAAGACACACTTCTACTAACCAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGACTCTAACCCAGCTACTTTCCCATTTGAACGCTACTTTGACGCTGACTTCTCT 1080
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QY 1081 CAGCACAACTATGTTTCTATTTCCTGCTTTGGGTTTGTACACGGTACTAAGCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY 1141 TTGCTACTACTTCTGTTGAACTATTGAGAACTGACGGTACTCTCTCTCTTGGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY 1201 GTTCCATCTCCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1261 TTGGTTAGAGTTTGGTTAAGCAGAGAGTTGTTCCATTGACGGTTGTGGTGTGACAGAC 1320
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QY 1321 TTGGGTAGATCTAGACAGACGACTTCGTTGAGGTTTGTCTTTCCTAGATCTGGTGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

QY 1381 AACTGGGAAGAATGTTTCGCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465
RESULT 5
US-10-213-990-24
: Sequence 24, Application US/10213950
: Publication No. US20030082595A1
: GENERAL INFORMATION:
: APPLICANT: Jiang, Bo
: APPLICANT: Bussey, Howard
: APPLICANT: Storms, Reg
: APPLICANT: Roemer, Terry
: TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
: TITLE OF INVENTION: ENZYMES AND METHODS OF USE
: FILE REFERENCE: 10182-019-999
: CURRENT APPLICATION NUMBER: US/10/213,990
: CURRENT FILING DATE: 2002-08-05
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24
: LENGTH: 474
: TYPE: PRT
: ORGANISM: Aspergillus
US-10-213-990-24
Alignment Scores:
Pred. No.: 3,44e-146 Length: 474
Score: 1881.50 Matches: 355
Percent Similarity: 84.76% Conservative: 40
Best Local Similarity: 76.18% Mismatches: 64
Query Match: 75.68% Indels: 7
Gaps: 2
US-09-488-265b-30 (1-1404) x US-10-213-990-24 (1-474)
QY 4 GGGCTGTTCTCGTGTACTGCTCCATTGCCACCTGTTGCGTTCACATCCGGTACCGCC 63
Db 16 GlyAlaValValleuIleuLysArgSerArgValSerAlaAlaProSerSer----- 33
QY 64 TTGGGTCTCGTGGTAACTCTCTGTGACACTGTTGACGGTGTGTTACCAATGTTTC 123
Db 34 -----AlaGlySerLysSerCysAspThrValAspLeuGlyTyrGlnCysSer 49
QY 124 CCAGAAATTTCTCACTGTTGGGTATACCTCTCCATTCTCTCTTGGCTGACCAATCT 183
Db 50 ProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeu 69
QY 184 GCTATTCTCCAGACGTTCCAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCTAGA 243
Db 70 SerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSerArg 89
QY 244 CAGGTGCTAGATACCAACTTCTTCTGCGTCTAAGCGTACTCTGCTTGTGATTGAGCT 303
Db 90 HisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThrAla 109
QY 304 ATTCAAAGAACGCTACTGCTTTCAAGGGTAACTAGCTTCTTGAAGACTTACAACTAC 363
Db 110 IleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyr 129
QY 364 ACTTTGGGTGCTGACGACTTGTACTCCATTGGGTGAACAACAAATGGTTAACTCTGTTAT 423
Db 130 ThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIle 149
QY 424 AAGTCTACAGACATACAAAGGCTTGGGTAGAAAGATTGTTCCATTTCATTACAGCTTCT 483
Db 150 LysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAlaSer 169
QY 484 GTTCTCACAGAGTATTGCTTCTGCTGAAAGCTTCAATGAAGCTTCCAAATCTGCTAG 543
Db 170 GlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLys 189

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QY 544 TTGGCTGACCGAGGTGCTAACCCACCAAGCTCTCCAGTTATTAACGTTATTTCCA 603
Db 190 LeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIlePro 208
QY 604 GAAGGTGCTGGTTACAAACACACTTTGGACCAAGGTTTGTGCTACTGCTTTGGAAGAICT 663
Db 209 GluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAlaSer 228
QY 564 GAATTGGGTGACGACGCTGAAGCTAACTCACTGCTGCTGTTTTCGCTCCACCAATTAGAGCT 723
Db 229 GluLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAla 248
QY 724 AGATTGGAAGCTCACTTGCAGGCTGTTAACTTGACGACGAAGAGCTGTGTTAACTTGATG 783
Db 249 ArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeuMet 268
QY 784 GACATGTGCTCACTGACACTGCTCTGAGAACTCTGACGCTACTCAATTCCTCCATC 843
Db 269 AspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerProPhe 286
QY 844 TGTGACTTGTCTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAAG 903
Db 289 CysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLys 308
QY 904 TACTAGGTTACGGTCTGCTGTAACCATTTGGGTCCAGCTCAAGGTGTTGGTTTGGTTAAC 963
Db 309 TyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsn 328
QY 964 GAATTGATTGCTAGATTGACTCACTTCCAGTTCAGACCAACACACTTCTACTCAACACAC 1023
Db 329 GluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSerThr 348
QY 1024 TTGACTCTAAACCCACTACTTCCCATTTGACGCTACTTTGTAGCTGACTTCTCTCAC 1083
Db 349 LeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSerHis 368
QY 1084 GACAACACTATGGTTCTATTCTTCGCTTTGGGTTTGTACAAAGGTTACTAAAGCCATTG 1143
Db 369 AspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeu 388
QY 1144 TCTACTACTTCTTGAATCTATTGAGAACTAGCGGTACTCTGCTTCTTGACTGTT 1203
Db 389 SerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValVal 408
QY 1204 CCATTGCTCTAGACCTTACGTTGAATGATGCAATGATGAAGCTGAAGAAAGAACCATIG 1263
Db 409 PropheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluProLeu 428
QY 1264 GTTAGACTTTTGGTTAACGACAGAGTGTCCATTGCCAGGTTGGTGTGTGACAGTTG 1323
Db 429 ValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLysLeu 448
QY 1324 GGTAGATGTAAGAGACGACTTCTGTTGAAGTTTGTCTTTGCTAGATCTGGTGGTAAC 1383
Db 449 GlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyCysAsn 468
QY 1384 TGGGAAGAATGTTTCGCT 1401
Db 469 TrpGlyGluCysPheSer 474
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RESULT 6

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US-10-062-848-80
; Sequence 80: Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WISS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
```

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; CURRENT APPLICATION NUMBER: US/10/062.848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PRI
; ORGANISM: Aspergillus fumigatus
; US-10-062-848-80

Alignment Scores:
Pred. No.: 4,54e-146 Length: 465
Score: 1880.00 Matches: 358
Percent Similarity: 84.15% Conservative: 35
Best Local Similarity: 76.66% Mismatches: 72
Query Match: 75.62% Indels: 2
DB: 15 Gaps: 2

US-09-488-265B-30 (1-1404) x US-10-062-848-80 (1-465)
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QY 1 ATGGCGGTGTTGCGTCTGCTACTGTCCATTCGCCACCTTGTTCGGTCCCAICCGGTACC 60
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 61 GCCTTGGTCTCGTGTAACTCTCACTCTTGTGACACTGTTCACGGTGTGTACCAATGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TTCACAGAAATTCACATCTGTGGGTACATACATCTCCATCTCTCTTGGCGTACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCAGACGCTTCCAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 ACACACGGTGTAGATACCCAACTTCTTCGGTCTAAGGCGTACTCTGCTTTCATGAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99
QY 301 GCTATTTCAAAAGAACGCTACTGCTTTCAAAGGTAAAGTACGCTTCTTTCGAAGACTTACAAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTCGGTGTGACGACTTGACTCCATTCGGTGAACACAAATGSGTTAACICTGGT 420
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAGTCTTACAGAGATACAAAGCTTGGCTGAAGAAGATTGTTCACATTCATITAGAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGTTCTGACAGAGTTATTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
QY 541 AAGTTGGCTGACCCAGGTGCTTAACCCACACAAAGTCTCTCCAGTTATTATTAATTTATT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAAAGTGTGGTTTACAAACACACTTTGGACCAAGGTTTGTGCTACTGCTTTCGGAAGAA 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTCGGTGACGACTGCAAGCTAACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAAGCTCACTTGCAGGTTGTTAACTTGTACTGACGAGACGTTGTTAACTTG 780
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239	AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu	258
781	ATGGACATGTTGTCATTTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATCTCTCTCCA	840
259	MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro	279
841	TTCTGTGACTTGTTCACCTACGACGCAATGGATTCATACGACTACTTCGCAATCTTTGGT	900
279	PheCysGlnLeuPheThrHisAsnGluTrpLysLysIleValAsnIleLeuGlnSerLeuGly	298
901	AACTACTACGGTTACGTTGGTGAACCCATTGGGTCAGCTCAAGGTTGGTTTCCTT	960
299	LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr	318
961	AAAGAAATGATTGCTACATGACTCACTCTCCAGTTCAGACCACACTTCTTACTAACCC	1020
319	AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer	338
1021	ACTTTGGACTCTAACCCAGCTACTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCT	1080
339	ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer	356
1081	CACGACACACTATGGTTTCTATTCTTCGCTTGGGTTTGTACAAAGCGTACTAACCCA	1140
359	HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro	378
1141	TTGCTACTACTTCTGTGTAATCTATTGAAGAACTGACGGTTACTCTGCTCTCTGGACT	1200
379	LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal	398
1201	GTTCATTTCGCTCGTACAGCTTACGTTGAATCATGCAATGTGAGCTGAAAGACCA	1260
399	ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluSer	418
1261	TTGGTTAGAGTTTGGTTAAACACAGAGTTGTTCATTGACGGTTGGTGTGTGACAAG	1320
419	LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys	436
1321	TTGGGTAGATGATAGACAGGACTTCGTTGAAGGTTGTCTTTCGCTAGATCTGGTGGT	1380
439	LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly	458
1381	AACTGGGAAGAATGTTTCGCT	1401
459	AsnTrpGlyGluCysPheSer	465

RESULT 7

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US-10-062-848-79
: Sequence 79, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062.848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 79
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-10-062-848-79

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Alignment Scores:			
Pred. No.:	5,48e-146	Length:	465
Score:	1879.00	Matches:	358
Percent Similarity:	84.15%	Conservative:	35
Rest Local Similarity:	76.66%	Mismatches:	72
Query Match:	75.58%	Indels:	2
DB:	15	Gaps:	2
CS-09-488-265B-30 (1-1404) x US-10-062-848-79 (1-465)			
Qy	1	ATGGGGCGTGTTCGTGGTGCTACTGTCCATTGCCACITGTTCCGTTCCACATCCGGTACC	60
Ds	1	MetValThrLeuThrPheLeuLeuSerAlaAlaLafyrLeuLeuSerGlyArgValSerAla	20
Qy	61	GCCTTGGGCTCGTGGTAACACTCTCACCTCTGTGACACTGTTGACGGTGGTACCAATGT	120
Ds	21	AlaProSerSerAlaGly---SerLysSerCysaspThrValAspLeuGlyTyrGlnCys	39
Qy	121	TTCCAGAAATTTCTCACTTTGGGGTACATACTTCCATTCTCTCTTTGGCTGACGAA	180
Ds	40	SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu	59
Qy	181	TCGTCTATTCTCCAGACGITCCAAAGGGTGTACAGTAACTTTCTCGTTCAGTTTGTCT	240
Ds	60	LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer	79
Qy	241	AGACACGGTCTAGATACCAACTTCTCTCGCTTAAGGGTACTCTGCTTTTCATTCAA	300
Ds	80	ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysIlyrLysLysLeuValThr	99
Qy	301	GCTATTCAAAGACGCTACTGCTTTCAGGGTAGTAGCGCTTCTTGAAGACHTACAAC	360
Ds	100	AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn	119
Qy	361	TACACTTTGGGTGCTGACGACTTGACTCCATTCCGTTGAACAACTGGTTAACTCTGGT	420
Ds	120	TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnLeuValAsnSerGly	139
Qy	421	ATTAGTCTTACAGAAGATACAGGCTTGGCTAGAAAGATTTGTCATTTCATTAGAGCT	480
Ds	140	IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValProPheIleArgAla	159
Qy	481	TCGTGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTTCATTGAAGGTTTCCATCTCT	540
Ds	160	SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla	179
Qy	541	AGTGTGGCTGACCCAGGTCTTAACCCACACCAAGCTTCTCCAGTTATTTCAGTTATT	600
Ds	180	LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle	199
Qy	601	CCAGAAGGTGCTGGTTACAAACACACTTTGACACCGTTTGTGTACTGCTTTCGAAGAA	660
Ds	199	ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla	218
Qy	661	TCTGAATGGGTGACAGCTGTGAAGCTTAACCTCACTGCTGTTTTCGCTCCACCAATTAGA	720
Ds	219	SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg	238
Qy	721	GCTAGATTGGAAGCTCACCTTGCACCGTGTAACTTTGACTGACGAAGAGGTGTAACTTG	780
Ds	239	AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValSerLeu	258
Qy	781	ATGGACATGTGTCATTGACACTGTTGCTAGAACTTCTGACGCTACTCAATGTCTCCA	840
Ds	259	MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro	278
Qy	841	TTCGTGACTTGTTCCTCACACCAATGGATTCAATACGACTACTTGCATCTTTGGGT	900
Ds	279	PheCysGlnLeuPheThrHisAsnGluTrpLysIlyrAsnIlyrLeuGlnSerLeuGly	298
Qy	901	AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTGTTTTCGTT	960


```

: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 81
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Alignment Scores:
Pred. No.: 9,68e-146 Length: 465
Score: 1876.00 Matches: 357
Percent Similarity: 84.15% Conservative: 36
Best Local Similarity: 76.45% Mismatches: 72
Query Match: 75.46% Indels: 2
DB: 15 Gaps: 2

US-09-488-265b-30 (1-1404) x US-10-062-848-81 (1-465)

QY 1 ATGGCGGCGTCTCGTCTGCTACTGCTCCATTCGACCTTGTTCGGTCCACATCCGGTACC 60
Db MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 61 GCCTTGGGTCCTCGGTAACTCTCACCTCTTGACACTGTGACGGTGGTACCAATGT 120
Db AlaProSerSerAlaGly--SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TTCCCAAGAAATTCTCACTTGTGGGTACATACCTCCCATCTTCTCTTCTTGGCTGACGAA 180
Db SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCAGACCTTCCAAAGGGTGTGACAGTACTTTCGTTCAAGTTTGHCT 240
Db LeuSerValSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACAGGTCGTAGATACCAACTCTCTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99
QY 301 GCTATTCAAAGACCTACTCTCTTCAGGGTAACTACCGCTTCTTGAAGACTTACAC 360
Db AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 159
QY 361 TACACTTTGGGTCTGACGACTTGACTCCATTCGGTGAACAAATGGTTAACTCTGCT 420
Db TyrThrLeuGlyAlaAspLeuThrAlaPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTCTACAGAGATACAGGCTTTGGCTAGAAGATTGTTCCATTTCATTAGACT 480
Db IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGGTCTTCACAGACTTATGCTCTGCTGAAAAGTTCATTGAAGGTTTCCATCTGCT 540
Db SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179
QY 541 AAGTTGGCTGACCCAGGTCTAACCCACACCAAGCTTCTCCAGTTATTAAAGCTATTATT 600
Db LysLeuAlaAspProGlyAlaThr--AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAGAGTCTGTTTACACACACACTTTGGACCCAGGTTTGTGACTGCTTTTCGAAGA 660
Db ProGluSerGluThrPheAsnAsnThrLeuAspPheIleValCysThrLysPheGluAla 218

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661 TCTGAATTGGGTGACGAGGTGACAGCTTAACCTAACTTCACTGCGTGTTCGCTCCACCANTAGA 720
Db SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
721 GCTAGATTGGAAGCTCACITGCCAGGTCTTAACCTTGAAGTGAAGACGCTGTTTAAGCTTG 780
Db AlaArgAlaLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
781 ATGGCATGTGTCCAATCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTTGCTCCA 840
Db MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
841 TTCTGTGACTTGTTCACCTCAGCACAATGGATTCAATACGACACTTTCATCTTTGGGT 900
Db PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
901 AAGTACTACGGTTACGGTGTGTAACCCATTGGTCCAGCTCAAGGTGTGTGGTTTCGTT 960
Db LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
961 AACGAATTGCTAGATTGACTCCTCCTCAGTTCAGGTTCAAGACACACTTCTTACTAACCA 1020
Db AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
1021 ACTTTGGACTCTAACCCAGCTACTTTCCTCATTTGAAGCTGACTTGTGACGCTGACTTCT 1080
Db ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
1081 CACGACACACTATGTTTCTATTTCCTTCGCTTGGGTTTCTTACAAGGTTACTAAGCCA 1140
Db HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
1141 TTCTCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerIleVal 398
1201 GTTCCATTGCTGCTAGAGCTTACGTTCAATGATGCAATGATGCAAGCTGAAAGGACCA 1260
Db ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
1261 TTGGTTAGAGTTTGGTTAACGACAGCTGCTTCATTGACGGTTGCTGTTGACGAG 1320
Db LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
1321 TGGGTAGATGTAAGACGACGACTTGGTTGAAGGTTTCTTTCGCTAGATGCTGGTGGT 1380
Db LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
1381 AACTGGGAAGAATGTTCCCT 1401
Db AsnTrpGlyGluCysPheSer 465

RESULT 11
US-10-062-848-82
: Sequence 82, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 82
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-82

Alignment Scores:
Pred. No.:      6,27e-144      Length:      469
Score:          1854.00      Matches:      347
Percent Similarity: 84.47%      Conservative: 50
Best Local Similarity: 73.83%      Mismatches: 69
Query Match:      74.58%      Indels:      4
DB:              15      Gaps:      2

US-09-488-265B-30 (1-1404) x US-10-062-848-82 (1-469)

QY      1  ATGGCGGTTCGGTGGTCTACTGTCCTCCACCTTGTCGGTTCACATCCGGT--- 57
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Db      1  MetGlyAlaLeuThrPheLeuLeuSerValMetTyrLeuLeuSerGlyValAlaGlyAla 20
QY      58  -----ACGGCTCGGTCCGGTGAACCTCCTACCTCTTGACACTGTTGTGACAGCTGGT 111
      |||||
Db      21  ProSerSerGlyCysSerAlaClySerGlySerLysAlaCysAspThrValGluLeuGly 40
QY      112  TACCAGTTCCTCCAGAAATTCCTACCTGTGGGTACATCTCTCCATTCTCTCTCTG 171
      |||||
Db      41  TyrGlnCysSerProGlyThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeu 60
QY      172  GGTACGAATCTGCTATTCTCCAGACGCTTCCAAAGGCTTGAGAGTACTTCTGCTCAA 231
      |||||
Db      61  GluAspGluLeuSerValSerSerAspLeuProLysAspCysArgValThrPheValGln 40
QY      232  GTTTGTCTAGACGCGTCTAGATACCACTCTCTCTGCTCTAAGCGCTACTCTGCT 291
      |||||
Db      81  ValLeuSerArgHisGlyAlaArgTyrProThrAlaSerLysSerLysLysTyrLysLys 100
QY      292  TTGATTGAAGCTATTCAAAGAACGCTACTGCTTTCAAGGGTGAAGTACTTCTTGAAG 351
      |||||
Db      101  LeuValThrAlaIleGlnLysAsnAlaThrGluPheLysGlyLysPheAlaPheLeuGlu 120
QY      352  ACTTACACTACACTTGGGTCTGACGACTGACTCCATTCGGTGAACACAATGGTT 411
      |||||
Db      121  ThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnMetVal 140
QY      412  AACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTGGCTAGAAAGATTGTTCCATTC 471
      |||||
Db      141  AsnSerGlyLysPheTyrGlnLysTyrLysAlaLeuAlaGlySerValValProPhe 160
QY      472  ATTAGAGCTTCTGGTCTGACAGAGTTATTGCTTCTGCTGAAAGTTCATTGAAGTTTC 531
      |||||
Db      161  IleArgSerSerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPhe 180
QY      532  CAATCTGCTGAAGTCTGCTGACCGAGTCTAACCACACACAGCTTCTCCAGTTATTAC 591
      |||||
Db      181  GlnGlnAlaAsnValAlaAspProGlyAlaThr---AsnArgAlaAlaProValIleSer 199
QY      592  GTATTATTCCAGAGTGTGGTACACACACTTTGGACCCAGGTTTGTGTACTGCT 651
      |||||
Db      200  ValIleProGluSerGluThrTyrAsnAsnThrLeuAspHisSerValCysThrAsn 219
QY      652  TTCGAAGAATCTGAATTGGTGGACAGCTTGAAGCTAATCTTCACTGCTGTTTTCGCTCA 711
      |||||
Db      220  PheGluAlaSerGluLeuGlyAspGluValGluAlaAsnPheThrAlaLeuPheAlaPro 239
QY      712  CCAATTAGACTAGATTGGAACCTCAGTCCGAGCTGTTAATCTGACACACCAAGCTTT 771
      |||||
Db      240  AlaIleArgAlaArgIleGluLysHisLeuProGlyValGlnLeuThrAspAspVal 259
QY      772  GTTAACCTGATGACATGTGCTCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAA 831
      |||||
Db      260  ValSerLeuMetAspMetCysSerPheAspThrValAlaArgThrAlaAspAlaSerGlu 279
QY      832  TTGCTCTCCATTCTGTGACTTGTCTACTCACGACGAATGGAATCAATACGACTACTTCAA 891
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Db      280  LeuSerProPheCysAlaIlePheThrHisAsnGluThrPlyLysTyrAspTyrLeuGln 299
QY      892  TCITTTGGGTAAGTACTACGCTTACGGTCTGGTGAACCCATTTGGGTCCAGCTCAAGTGTT 951
      |||||
Db      300  SerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIle 319
QY      952  GGTTCGTTAACCAATTTGATGCTAGATTGACTCTCTCCAGTTTCAAGACCACACTTCT 1011
      |||||
Db      320  GlyPheThrAsnGluLeuIleAlaArgLeuThrAsnSerProValGlnAspHisThrSer 339
QY      1012  ACTAACCCACACTTTGGACTCTAACCCAGCTACTTCCCATTTGAACGCTACTTGTACGCT 1071
      |||||
Db      340  ThrAsnSerThrLeuAspSerAspProAlaThrPheProLeuAsnAlaThrIleTyrVal 359
QY      1072  GACTTCTCTCAGACACACTACTGTTTCTATTCTTCTGCTTGGGTTTGTACACGGT 1131
      |||||
Db      360  AspPheSerHisAspAsnGlyMetIleProIlePheAlaMetGlyLeuIleAsnGly 379
QY      1132  ACTAAGCCATTTGCTACTTCTGTTGAATCTATTGAAGAAACAGAGGTTTACTCTGCT 1191
      |||||
Db      380  ThrGluProLeuSerGlnThrSerGluGluSerThrLysGluSerAsnGlyTyrSerAla 399
QY      1192  TCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGAATGATGCAATGTGAAGTGAA 1251
      |||||
Db      400  SerTrpAlaValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGlu 419
QY      1252  AAGAACCATTTGGTGTAGAGTTTGGTTTACGACAGAGTGTTCATTCATTCGACGGTGTG 1311
      |||||
Db      420  LysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAla 439
QY      1312  GTTGACAAAGTTGGTACATGCTAAGAGACGACTTCTGTTCAAGGTTTGTCTTTCGCTAGA 1371
      |||||
Db      440  ValAspLysLeuGlyArgCysLysLeuLysAspPheValLysGlyLeuSerTrpAlaArg 459
QY      1372  TCTGTTGGTAACTGGGGAAGTATTTGCT 1401
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Db      460  SerGlyLysAsnSerGluGlnSerPheSer 469

RESULT 12
US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbia
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
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221 ScrguLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

721 GCATGATTGGAGCTCACITTCGCCAGGTGTTAACTTCGACTGACGACGACGCTGTTAACTTG 780

241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrIyrLeu 260

761 ATGGACATGCTGCATTCGACATGTTGCTAGAACCTTCTGACGCTACATTAATGTCCTCA 840

261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrIysLeuSerPro 280

841 TTCTCTGACTGTTTCACTCAGCAGCAATGATTCATACGACTACTTGCATCTTTGGT 900

281 PheCysAspLeuPheThrHisAspGluTrpIleAsnIyrAspIyrLeuGlnSerLeuLys 300

901 AAGTACTACGGTTACGGTGTGTAACCCATCGGTCACAGCTCAAGGTGTGGTTCCT 960

301 LysTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyIyrAla 320

961 AACGAATTGATTGCTAGATTGACTCACICTCCAGTTCAAGACCACACACTCTCTACTAAC 1020

321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspThrSerSerAsnHis 340

1021 ACTTTGGACTCTAACCCAGCTACTTCCCATTTGAAGCTACTTTGTACGCTGACTTCTCT 1080

341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

1081 CAGCACACACTATGGTTTCTATTCTTCGCTTGGTTCGGTTCGCTGACTTAAGCCA 1140

361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrIysPro 380

1141 TTGCTACTACTTCTGTGTAATCTATTGAAGAACTACGCGGTTCCTCTGCTTTGGACT 1200

381 LeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCATTGCTGCTAGACCTTACGTTGAATCATGCAATGTGAAGCTGAAAGGAACCA 1260

401 ValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGlnGluPro 420

1261 TTGGTTAGAGTTTGGTTTAAACGACAGAGTTGTTCCATTGCACGGTGTGCTGTCACA 1320

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1321 TTGGGTAGATGTACAGAGACGACCTCGTTGAAGGTTTGTCTTCGCTAGATCTGGTGGT 1380

441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

1381 AACTGGGAAGATGTTTCCT 1401

461 AspTpaGluCysPheAla 467

RESULT 13

US-10-229-358-5

Sequence 5, Application US/10229358

Publication No. US20030124700A1

GENERAL INFORMATION:

APPLICANT: Stafford, Christian F.

APPLICANT: Irinci, Anthony P.J.

TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding

TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating

FILE REFERENCE: GC586-2

CURRENT APPLICATION NUMBER: US/10/229,358

CURRENT FILING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: US 60/148,960

PRIOR FILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 467

TYPE: PRT

ORGANISM: Aspergillus niger

US-10-229-358-5

Alignment Scores:

Pred. No.: 1,95e-143 Length: 467
Score: 1848.00 Matches: 347
Percent Similarity: 83.30% Conservative: 42
Best Local Similarity: 74.30% Mismatches: 78
Query Match: 74.34% Indels: 0
DB: 15 Gaps: 0

US-09-488-265B-30 (1-1404) x US-10-229-358-5 (1-467)

QY 1 ATGGGCGTGTTCGTGCTGCTACTGTCCATIGCCACCTGTTCGGTTCACATCCGGTACC 60
DB 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20
QY 61 GCCTTGGGTCCTCGTGGTCACTCTCTGTGACACTGTTCGAGGGTGGTTACCAATGT 120
DB 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TTCCAGAAATTTCTCACTTGTGGGTGATACACTCTCCATCTCTCTTTCGCTGACGAA 180
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QY 181 TCTGCTATTCTCCAGACGCTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
DB 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY 241 AGACAGGCTGTAGATACCAACTCTTCTCGGCTTAAGGCTGCTACTCTGCTTGTATTGAA 300
DB 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGAACGCTACTGCTTTCAAGGGTGAAGTACTGCTTCTTGAAGCTTACAC 360
DB 101 GluIleGlnGlnAsnAlaThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTTGGGTGCTGACAGCTGACTCCATTCGTTGCGTGAACAACAATGGTTAACTCTGT 420
DB 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAAGTCTACAGAGATACAGGCTTTGGCTAGAAAGATTGTCCATTCAITAGACT 480
DB 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 481 TCTGGTCTCACAGAGTATTGCTGCTGCTGAAAGTTCAITGAAGTTTCCAACTCTCT 540
DB 161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180
QY 541 AAGTTGCTGACCCAGGTGCTACCCACACCAAGCTTCTCCAGTTATTAACTGTTATT 600
DB 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle 200
QY 601 CCAGAAGTGTCTGTTACAAACACACTTTGGACCCAGGTTTGTGTACTCTCTTCAAGAA 660
DB 201 SerGluAlaSerSerSerAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATTTGGGTGACGAGTTGAAGCTTAACCTGCTGTTTTCGCTCCACCAATTAGA 720
DB 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 721 GCTAGATTGGAAGCTCACTTGCACGAGTGTAACTTGTACTGACCAAGACCTTGTAACT 780
DB 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
QY 781 ATGACATGTGCTCATTCGACACTGTTGCTGAGAACCTTCTGACGCTACTCAATGTCTCA 840
DB 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
QY 841 TCTGCTGACTTGTCTACACGAGATGATTCATATACAGACTACTTGCATCTTGGGT 900
DB 281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
QY 901 AAGTACTACGTTACGCTGCTGCTGATCCCATTCAGCTTGGTCCAGCTCAAGTGTGCTT 960
DB 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGluProThrGlnGlyValGlyTyrAla 320

QY 561 AACGAATGATTGCTAGATTGACTCTCAGTTCAGGTTCAAGACACACACTTCTACTAACCA 1020
DB 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspThrSerSerAsnHis 340
QY 1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTTGAAGAGCTACTTTGACGCTGACTTCT 1080
DB 341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
QY 1081 CAGCAACACACTATGTTCTTCTTTCTGCTTGGGTTGTGACAGGTTACTAAGCA 1140
DB 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
QY 1141 TTGCTACTACTTCTCTGAACTTATTGAAGAACTGACGGTACTCTGCTTCTTGGACT 1200
DB 381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
QY 1201 GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCTCAATGTGAAGCTGAAAGCAACA 1260
DB 401 ValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGluGlnGluPro 420
QY 1261 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCATTCACGGTTGTGGTGTTCGACAG 1320
DB 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
QY 1321 TTGGTAGATGTAAGACAGACGACTTCGTTGAAGTTTGTTCGCTAGATCTGTTGCT 1380
DB 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGAAGAATGTTTCGCT 1401
DB 461 AspTrpAlaGluCysPheAla 467

RESULT 14
US-09-929-060-3
Sequence 3, Application US/09929060
Patent No. US20020068350A1
GENERAL INFORMATION:
APPLICANT: KONDO, HIROMASA
APPLICANT: ANAZAWA, HIDEHARU
APPLICANT: KANEKO, SYUNICHI
APPLICANT: NAGASHIMA, TADASHI
APPLICANT: TANGE, TATSUYA
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 081356/0166
CURRENT APPLICATION NUMBER: US/09/929,060
PRIOR FILING DATE: 2001-08-05
PRIOR APPLICATION NUMBER: 09/543,744
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 09/155,855
PRIOR FILING DATE: 1998-10-05
PRIOR APPLICATION NUMBER: JP 084314/1996
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 467
TYPE: PRT
ORGANISM: Aspergillus niger
US-09-929-060-3

Alignment Scores:
Pred. No.: 7,34e-143 Length: 467
Score: 1841.00 Matches: 342
Percent Similarity: 83.73% Conservative: 49
Best Local Similarity: 73.23% Mismatches: 76
Query Match: 74.05% Indels: 0
DB: 9 Gaps: 0

US-09-488-265B-30 (1-1404) x US-09-929-060-3 (1-467)

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DB 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20
QY 61 GCCTTGGGTCCTCGTGGTCACTCTCTGTGACACTGTTCGAGGGTGGTTACCAATGT 120
DB 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TTCCAGAAATTTCTCACTTGTGGGTGATACACTCTCCATCTCTCTTTCGCTGACGAA 180
DB 41 PheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
QY 181 TCTGCTATTCTCCAGACGCTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
DB 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY 241 AGACAGGCTGTAGATACCAACTCTTCTCGGCTTAAGGCTGCTACTCTGCTTGTATTGAA 300
DB 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGAACGCTACTGCTTTCAAGGGTGAAGTACTGCTTCTTGAAGCTTACAC 360
DB 101 GluIleGlnGlnAsnAlaThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTTGGGTGCTGACAGCTGACTCCATTCGTTGCGTGAACAACAATGGTTAACTCTGT 420
DB 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAAGTCTACAGAGATACAGGCTTTGGCTAGAAAGATTGTCCATTCAITAGACT 480
DB 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 481 TCTGGTCTCACAGAGTATTGCTGCTGCTGAAAGTTCAITGAAGTTTCCAACTCTCT 540
DB 161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180
QY 541 AAGTTGCTGACCCAGGTGCTACCCACACCAAGCTTCTCCAGTTATTAACTGTTATT 600
DB 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle 200
QY 601 CCAGAAGTGTCTGTTACAAACACACTTTGGACCCAGGTTTGTGTACTCTCTTCAAGAA 660
DB 201 SerGluAlaSerSerSerAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATTTGGGTGACGAGTTGAAGCTTAACCTGCTGTTTTCGCTCCACCAATTAGA 720
DB 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 721 GCTAGATTGGAAGCTCACTTGCACGAGTGTAACTTGTACTGACCAAGACCTTGTAACT 780
DB 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
QY 781 ATGACATGTGCTCATTCGACACTGTTGCTGAGAACCTTCTGACGCTACTCAATGTCTCA 840
DB 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
QY 841 TCTGCTGACTTGTCTACACGAGATGATTCATATACAGACTACTTGCATCTTGGGT 900
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QY 901 AAGTACTACGTTACGCTGCTGCTGATCCCATTCAGCTTGGTCCAGCTCAAGTGTGCTT 960
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QY 181 TCTGCTATTCTCCAGACGCTCCAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
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QY 301 GCTATTCAAGAAGCGTACTGCTCTCAAGGTAAGTACGGTTTCTGAAGACATTACAC 360
Db 101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrIleArg 120
QY 361 TACACTTGGGTGCTGACGACTTGACTCCATTCCGTTGAACAACTGTTAACTCTGCT 420
Db 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAAGTTCTACAGAGATACAGGCTTTGGCTAGAAAGATTGTTCCATTCAATAGACT 480
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QY 481 TCTGGTCTCGACAGAGTATTGCTCTGCTGCTGAAAGTTCAITGAAGGTTTCCAACTGCT 540
Db 161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180
QY 541 AAGTTGGCTGACCCAGGTCCTAACCCACACCAAGCTTCTCCAGTTATTAAAGTTAATT 600
Db 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200
QY 601 CCAGAGGTGCTGGTTACAAACACACTTTGGACACAGGTTTGCTGACTGCTTTCGAAGA 660
Db 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATTGGGTGACGACGCTTGAAGCTTAACITCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 721 GCTAGATTGGAGCTCACTTGCACGCTGTTTACITGACTGACGAGAGAGGTTGTTAACTTG 780
Db 241 GlnArgLeuGluAlaAsnLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
QY 781 ATGGACATGCTCCACTTCCACACTGTGTCTACAACTTCTGACGCTACTCAATTGCTCCA 840
Db 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
QY 841 TCTGTGCTACTGTTCTACTCACCAGCAATGATTCATATACAGCTACTTCCAACTTTGGGT 900
Db 281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
QY 901 AAGTACTAGGTTACGGTCTGTAACCCATTGGCTCCAGCTCAAGGTTGTTGGTTTGGTT 960
Db 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY 961 AACGAATTGATTGCTAGATTGACTCCTCCAGTTCAAGACCACTTCTACTAACCCAC 1020
Db 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340
QY 1021 ACTTTGGACTCTAACCCAGCTTCTCCATTGACGCTACTTTGTAGCTGACTTCTCT 1080
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QY 1081 CAGCAACACTATGTTCTATTCTTCTCGCTTGGGTTTGTACACGGTACTAAGCCA 1140
Db 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
QY 1141 TTGCTACTACTTCTGTGAACTATTGAAGAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db 381 LeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
QY 1201 GTTCCATTGCTGCTAGAGCTTACGTTGAATGATGCAATGTAAGCTGAAAGGAACCA 1260
Db 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluAlaPro 420

QY 1261 TTGGTTAGAGTTTGGTTAAAGACAGAGATTGTTCCATTGCACGGTTTCTGGTGTGACAAG 1320
Db 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
QY 1321 TTGGGTAGATGTTAAGACAGACGACTTGGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGAAGAATGTTTCGCT 1401
Db 461 AspTrpAlaGluCysPheAla 467

Search completed: October 3, 2003, 09:06:16
Job time : 54.6311 secs

Result No.	Score	Query %		Length	DB	ID	Description
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1	2308	92.8	467	4	US-09-273-871A-9	Sequence 9, Appl	
2	2182	87.8	441	3	US-09-121-425-1	Sequence 1, Appl	
3	2182	87.8	441	4	US-09-634-493A-1	Sequence 1, Appl	
4	2170	87.3	467	3	US-09-121-425-2	Sequence 2, Appl	
5	2170	87.3	467	4	US-09-634-493A-2	Sequence 2, Appl	
6	1888	75.9	465	3	US-08-868-435-33	Sequence 33, Appl	
7	1888	75.9	465	4	US-08-744-231-33	Sequence 33, Appl	
8	1888	75.9	465	4	US-09-044-718-78	Sequence 78, Appl	
9	1888	75.9	465	4	US-09-636-499-6	Sequence 6, Appl	
10	1888	75.9	465	4	US-09-273-871A-8	Sequence 8, Appl	
11	1880	75.6	465	4	US-09-044-718-80	Sequence 80, Appl	
12	1879	75.6	465	4	US-09-044-718-79	Sequence 79, Appl	


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QY 259 CCAACTCTCTCGCGTAAAGCGTACTCTGCTTTGATTGAAGCTATTCAAGAAGCGCT 318
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QY 319 ACTGCTTTCAAGGGTAAGTAGCGCTTCTTGAAGACTTACAACACTACACTTTGGGTGCTGAC 378
Db 81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100
QY 379 GACTTGACTCCANTTCGGTGAACAACAANATGGTTAACTCTGGTATTAACTTCTACAGAAGA 438
Db 101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg 120
QY 439 TACAAGGCTTGGCTAGAAAGATTCTCCATTCAATAGAGCTTCTGCTGTTCTGACAGACTT 498
Db 121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal 140
QY 499 ATTGCTTCTGCTGAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTCGGCTGACAGAGT 558
Db 141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160
QY 559 GCTAACCACACACCAAGCTTCTCCAGTTATTAACTGTTATTATTCAGAAGGTGCTGGTTAC 618
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Db 181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200
QY 679 GTTGAAGCTAACTTCACAGCTGTTTCGCTCCACCAATTAGAGCTAGATTGGAGAGCTCAC 738
Db 201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuAlaAsp 220
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Db 221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240
QY 799 GACACTGTGTGCTAGAACTTCTGACGCTACTCAATGTCTCCATTCTGTCGACTTGTTCACT 858
Db 241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260
QY 859 CACGACGAATGGATTCAATAGACTACTTGCAATCTTTGGTAACTACTAGGTTACGGT 918
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QY 919 GCTGTACCCANTGGGTCACGCTCAAGGTGTGTTGCTTAAAGAAATGATTCGCTAGA 978
Db 281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGlnLeuIleAlaArg 300
QY 979 TTGACTCACTCTCCAGTTCAAGACACACACTTCTACTAACCACACTTTGACCTCTAAACCCA 1038
Db 301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320
QY 1039 GCTACTTTCOCATTAAGCGCTACTTTGACGCTGACTTCTCTCAGCAACACACTAAGTGT 1098
Db 321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340
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Db 341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360
QY 1159 GAATCTATTGAAGAACTGACGCGTTACTCTGCTTCTGACTGTTTCCATTTCGCTGCTAGA 1218
Db 361 GluSerIleGluGluThrAspGlyTyrSerAlaSerThrThrValProPheCylAlaArg 380
QY 1219 GCTTACGTTGAAATGATCAATGTGAAGCTGAAAAGAACCACTTGGTTAGAGTTTTGTT 1278
Db 381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400
QY 1279 AACGACAGAGTTGTTCCATTGACCGGTTGTGCTGTGTGACAGAGTTGGCTAGAGTGAAGA 1338
Db 401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420
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QY 1339 GACGACTTCGTTGAAGGTTTGTCTTCGTAGATCTGCTGGTGAAGTGGGAAGATGTTTC 1398
Db 421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnThrAlaGluCysPhe 440
QY 1399 GCT 1401
Db 441 Ala 441
RESULT 3
US-09-634-493A-1
: Sequence 1, Application US/09634493A
: Patent No. 6579975
: GENERAL INFORMATION:
: APPLICANT: Lehmann, Martin
: TITLE OF INVENTION: Consensus Phytases
: FILE REFERENCE: consensus phytases 13239
: CURRENT APPLICATION NUMBER: US/09/634.493A
: PRIOR FILING DATE: 2000-08-08
: PRIOR APPLICATION NUMBER: US/09/121.425
: PRIOR FILING DATE: 1998-07-23
: PRIOR APPLICATION NUMBER: EPO 97112688.3
: PRIOR FILING DATE: 1997-07-24
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 441
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:consensus
US-09-634-493A-1
Alignment Scores:
Pred. No.: 1,73e-205 Length: 441
Score: 2182.00 Matches: 410
Percent Similarity: 95.46% Conservative: 11
Best Local Similarity: 92.97% Mismatches: 20
Query Match: 87.77% Indels: 0
Db: 4 Gaps: 0
US-09-488-265B-30 (1-1404) x US-09-634-493A-1 (1-441)
QY 79 AACTCTCACTCTTGACACTGTTGACGGTGTTCACCAATGTTTCCAGAAATTTCTCAC 138
Db 1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGluIleSerHis 20
QY 139 TTGTGGGTACATACTCTCCATTCTCTTCTTGGCTGACGAATCTGCTATTCTCCAGAC 198
Db 21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40
QY 199 GTTCCAAAGGTTTCTAGAGTTACTTTCGTTCAAGTTTGTCTAGACACGGTGTAGATAC 258
Db 41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr 60
QY 259 CCAACTTCTTCGCTGCTAAGCGTACTCTGTTGATTGAAGCTATTCAAAACAACGCT 318
Db 61 ProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla 80
QY 319 ACTGCTTTCAAGGGTAAGTAGCGCTTCTTGAAGACTTACAACACTACACTTTGGGTGCTGAC 378
Db 81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100
QY 379 GACTTGACTCCANTTCGGTGAACAACAANATGGTTAACTTCTGGTATTAACTTCTACAGAAGA 438
Db 101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg 120
QY 439 TACAAGGCTTGGCTAGAAAGATTGTTCCATTCAATAGAGCTTCTGCTGTTCTGACAGAGT 498
Db 121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal 140
QY 499 ATTGCTTCTGCTGAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTCGGCTGACAGAGT 558
Db 141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160
Db 161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr 180
Db 181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200
Db 201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuAlaAsp 220
Db 221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240
Db 241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260
Db 261 HisAspGluTyrArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280
Db 281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGlnLeuIleAlaArg 300
Db 301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320
Db 321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340
Db 341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360
Db 361 GluSerIleGluGluThrAspGlyTyrSerAlaSerThrThrValProPheCylAlaArg 380
Db 381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400
Db 401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420
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Db	141	IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly	160
QY	559	GCTAACCCACACCAAGCTTCTCCAGTTATTACGCTTATTATTCCAGAAGGTGCTGGTAC	618
Db	161	SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr	160
QY	619	AACACACTTTGGACCACGGTTTGTGTACTGCTTTTCGAAGATCTGAATTTGGGTGACGAC	678
Db	181	AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp	200
QY	679	GTTAGAGTCAACTTCACTGCTGTTTTCGGTCCACCACCAATTAGAGCTAGATTGGAAGCTCAC	738
Db	201	ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp	220
QY	739	TTCGACGCTTAACCTTCACTGACGACGAGCGTTGTTAACTTGTATGACATGTGTCCTATC	798
Db	221	LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe	240
QY	799	GACACGTTGCTAGAACTCTGACGCTACTCAATGTCTCCATTCTGCTCACTTGTCTCACT	858
Db	241	GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr	260
QY	859	CACGACGAATGGATTCAATACGACTACTTGCCAATCTTTGGGTAAGTACTACGGTTACGGT	918
Db	261	HisAspGluTyrAlaGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly	280
QY	919	GCTGGTACCCATTGGGTCCAGCTCAAGGTGGTTTCGTTTAAGCAATGATGCTCTAGA	978
Db	281	AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg	300
QY	979	TTGACTCACTCTCCAGTTCAAGACCACACTTCTTACTTAACACACACTTTGGACTCTAAACCA	1038
Db	301	LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro	320
QY	1039	GCTACTTTCCTTGAACGCTACTTTGTACGCTGACTTCTCTCAGCACACACTATGGTT	1098
Db	321	AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle	340
QY	1099	TCTATTTTCTTCGGTTTGGGTTTGTACAAGGCTACTAAGCCATTGTCTACTACTTCTGT	1158
Db	341	SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal	360
QY	1159	GAATCTATTGAAGAACTGACGGTTACTCTGCTTCTGGACTGTTCCTCATTCGCTCTAGA	1218
Db	361	GluSerIleGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg	380
QY	1219	GCTTACGTTGAAATGATCCAACTGGAAGCTGAAAGGAACCACTTGGTTAGAGTTTGGTT	1278
Db	381	AlaTyrValGluMetMetGlnCysGlnAlaGluGlyGluProLeuValArgValLeuVal	400
QY	1279	AACGACAGAGTTGTCCATTCACGGTTTGGTGTGTGACAAAGTTGGGTAGATGTAAGAGA	1338
Db	401	AsnAspArgValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg	420
QY	1339	GACGACTTCGTTGAAGGTTTCTTCCTCGCTAGATCTGGTGGTAACCTGGGAAGATGTTTC	1398
Db	421	AspAspPheValGluGlyLeuSerPheAlaArgSerGlyClyAsnTrpAlaGluCysPhe	440
QY	1399	GCT 1401	
Db	441	Ala 441	

RESULT 4

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: US-09-121-425-2
: Sequence 2, Application US/09121425
: Patent NO. 6153418
: GENERAL INFORMATION:
: APPLICANT: Lehmann, Martin
: TITLE OF INVENTION: Consensus Phytases
: FILE REFERENCE: consensus phytases 13239
: CURRENT APPLICATION NUMBER: US/09/121,425
: CURRENT FILING DATE: 1998-07-23
: EARLIER APPLICATION NUMBER: EPO 971112688.3

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QY 721 GCTAGATTGGAAGCTCACTTCCAGGTGTAACTTGAAGACGACGCTTGTACTTGG 780
Db 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
QY 781 ATGGACATGTCTCCATTCACACTGTGTGCTAGAACTTCTGACGCTACTCAATGTCTCCA 840
Db 261 MetAspMetCysProPheGluThrValAlaAArgThrSerAspAlaThrGluLeuSerPro 280
QY 841 TTCTGTGACTTGTCTCACTCAGCAGCAATGATTCATACGACTACTTGCATCTTGTGGT 900
Db 281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300
QY 901 AAGTACTACGGTACGGTCTGTACCACTTGGTCCAGCTCAAGGTGTGGTTCGTT 960
Db 301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320
QY 961 AACGAATGATGCTAGATTGACTCCTCCAGTTCACAGACACACTTCTACTAACCCAC 1020
Db 321 AsnGluLeuLeuAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340
QY 1021 ACITTTGGACTCTAACCCAGCTACTTCCCATTTGAACGGCTACTTGTACGCTGACTTCTC 1080
Db 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360
QY 1081 CACGACAACACTATGTTCTATTTCTTCTTCTGGTTCGCTTCTCAACCGTACTTAAGCCA 1140
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QY 1141 TTGCTACTACTTCTGTTGAACTATTTGAAGAACTGACGGTACTTCTGCTTCTTGGACT 1200
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QY 1201 GTTCCATTCGCTAGACCTTACGTTGAATGATGCAATGTGAACGCTGAAGGAAGCA 1260
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QY 1261 TTGGTTAGAGTTTGGTTAACCACAGAGTTGTTCATTCACCGGTTGTGGTCTTCACCAAG 1320
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QY 1321 TTGGGTAGATGTAAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGT 1380
Db 441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGAAGATGTTTCCT 1401
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RESULT 5

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US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634,493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-09-634-493A-2
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Alignment Scores:
Pred. No.: 2,69e-204 Length: 467
Score: 2170.00 Matches: 416
Percent Similarity: 87.68% Conservative: 11
Best Local Similarity: 85.42% Mismatches: 20
Query Match: 87.29% Indels: 40
Db: 4 Gaps: 2

US-09-488-265B-30 (1-1404) x US-09-634-493A-2 (1-467)
QY 1 ATGGGCGGTTCGTCGCTACTGTCATTCGCCACCTTGTTCGGTTCACATCCGGTACC 60
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QY 61 GCCTTGGGTCTCGTGGTAACTCTCACTCTTGTGACACTGTGTGACGGTGGTTACCAATGT 120
Db 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40
QY 121 TCCAGNAATTTCTACITCTGGGTACATCTCTCATCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
QY 181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTGTAGAGTTACTTTCTGTTCAAGTTTGTCT 240
Db 61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80
QY 241 AGACACGGTGTAGATACCCAACTCTCTGCGCTTAAGCGCTACTCTGCTTTGATTGAA 300
Db 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla----- 97
QY 301 GCTATTTCAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTCTTGAAGACTTACAAC 360
Db 96 -----ThrTyrAsn 100
QY 361 TACACTTTGGTGTGTCAGGACTTCACTCCATTCGGTCAACAAACAATGGTTAACTCTGGT 420
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QY 421 ATTAAGTCTTACACAAGATACAAAGCTTTGGCTAGAAGATTGTTCCATTATTAGACT 480
Db 121 IleLysPheTyrArgTyrGlyLysAlaLeuAlaArgLysIleValProPheIleArgAla 140
QY 481 TCTGGTCTGACAGATTATGCTTCTCTGCTGAAAGTTCAITGAAGTTTCCATCTGCT 540
Db 141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160
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Db 161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180
QY 592 -----GTTATTATT 600
Db 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200
QY 601 CCAGAAGGTGCTGTATACAAACACTTTGGACACCGTTTGTGCTGCTTTTCGAGAA 660
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QY 661 TCTGAATTTGGGTGACGAGCTTGAAGCTTAACCTCACTGCTCTGCTTTCGCTCCCAATAGA 720
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QY 721 GCTAGATTGAAGCTCACTTCCAGGTGTTAACTTGAAGTGTGCTGCTGCTGCTGCTGCT 780
Db 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
QY 781 ATGCACATGTCTCCATTCGACACTGTTGCTAGAACTTCTCAGCTACTCTCAATGTCTCCA 840
Db 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
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DB 301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320
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DB 321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340
QY 1021 ACTTTGGACTTACCAGCTACTTTCCCATTTGAAGCTACTTTGACGCTGACTTCTCT 1080
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QY 1321 TTGGTTAGAGTTAGAGAGAGCTTCGTTGAAGGTTTGTCTTCGCTAGATCTGTGGT 1380
DB 441 LeuGlyArgCysIysArgAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGAAGAATGTTTCGCT 1401
DB 461 AsnIlePalaGluCysPheAla 467

RESULT 6

US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221

GENERAL INFORMATION:

; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/868.435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/744,231
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: Case Docket 9339
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-2363

; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 104
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 374
; OTHER INFORMATION: /note="potential N-glycosylation site"
; US-08-868-435-33

Alignment Scores:

Align. No.: 1.29e-176 Length: 465
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservatives: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 3 Gaps: 2

US-09-488-265B-30 (1-1404) x US-08-868-435-33 (1-465)

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DB 21 AlaProSerSerAlaGly--SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TTCACAGAAATTCCTCACTTGTGGGTACATACTCTCCATTCTCTTTGGCTGACGAA 180
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QY 181 TCTGCTATTCTCCAGAGCTTCCAAAGGGTGTAGAGTACTTCTTCGTTCAAGTTTCTCT 240
DB 60 LeuSerValSerSerLeuLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACACGGTGTAGATACCCCAACTTCTTCGCTTAAGGCGTACTCTGCTTGAITCAA 300
DB 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99
QY 301 GCTATTCAAAGACGCTACTGCTTTCAGGGTGAAGTACGCTTCTTGAAGACTTACAAC 360
DB 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTGGTGTGACGACTTGTACTCCTTCGTTGAAGCAACAAATGGTAACTCTGGT 420
DB 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTTCTACAGAAGATACAAGCTTGTGGCTGAGAAGATTGTTCCATTATTAGACT 480
DB 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

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QY 481 TCTGTTCTGACAGAGTATTGCTTCTGCTGCAAGAGTTCATTTGAAGGTTCACATCTGCT 540
Db 160 SerGlySerArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179
QY 541 AAGTTGGCTGACCGAGGTGCTAACCCACACAGCTTCTCCAGTTATTAAAGTTATTATT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIle 198
QY 601 CCAGAGGTGCTGTTTACACACACTTTGGACACCGTTTGTCTACTGCTTTCGAAAGAA 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTTGGTGACGAGCTTGAAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 219 SerGlnLeuGlyAspGluAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
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Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
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Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TCTCTGACTTGTTCACACGACCAATGGATTCAATACGACTACTTCAATCTTGGGT 900
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Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
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Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CACGACACACTATGTTCTTATTTCTTCTGCTTGGGTTTGTACACGGTACTAAACCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
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RESULT 7

US-08-744-231-33

; Sequence 33, Application US/08744231

; Patent No. 6358722

; GENERAL INFORMATION:

; APPLICANT: Van Loon, Adolphus

; APPLICANT: Mitchell, David

; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY

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NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,231
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc_feature
LOCATION: 104
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 119
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LOCATION: 337
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NAME/KEY: misc_feature
LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-744-231-33
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Alignment Scores:
Pct. No.: 1,29e-176 Length: 465
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265B-30 (1-1404) x US-08-744-231-33 (1-465)

QY 1 ATGGGGGTGTTGCTGCTGCTACTGCTCAATGGCACCTTGTTCGTTCCACATCCGGTACC 60

Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

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QY 61 GCCTTGGTCTCGTGGTAACTCTCACTCTCTGTGACACTGTTGACGGTGGTTACCAATGT 120
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspGluGlyTrpGlnCys 39
QY 121 TCCCGAATAATTTCTCAGTCTGCGGGTACATCTCTCCATCTCTCTCTTGTGCTGACGAA 180
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
40 SerProAlaThrSerHisLeuTrpGlyGlnCysSerProPheSerLeuGluAspGln 59
QY 181 TCTGCTATTCTCCAGAGCTTCCAAAGGGTGTAGAGTACTTCTGCTTCAATTTTGTCT 240
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACACGGTCTAGATACCAACTCTCTCTGCGTCTAAGCGGTACTCTCTCTTTGATTGAA 300
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
80 ArgHisGlyAlaArgTrpProThrSerSerLysSerLysLysTrpLysLysLeuValThr 99
QY 301 GCTATTCAAAGAAGCGTACTGCTTCTCAAGGGTAACTAGCGTCTTCTTGAAGACTTACAA 360
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTrpAsn 119
QY 361 TACACTTGGGTGCTGACGACTTCACTCCATTCGGTGAACAAATGCTTAACCTCTGT 420
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTTCTACGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
140 IleLysPheTrpGlnArgIleLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGGTTCTACAGAGTATTGCTTCTGCTGAAAGTTCATGCAAGGTTTCCAATCTGT 540
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
QY 541 AAGTTGCTGACCCAGGTGTACCCACCAAGCTTCTCCAGTTATTAAAGGTTATTAT 600
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAAGGTGCTGGTTACACACACTTTGGACACGGTTTGTGCTACTGCTTTCGAAGAA 660
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTTGGTGACGAGTGAAGCTTAACCTCACTGCTGTTTTCGTCACCAATTAGA 720
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGAAGCTCACTTCCAGGTTTAACTTGAAGTCAAGGAGCGTTGTAACTTG 780
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGACATGTGTCCTCACTGACACTGTTGCTAGACACTTCTGACGCTACTCAATGTCTCCA 840
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TCTGTGACTTGTTCCTACGACGAGATGATTCATACGACTACTTGCATCTTTGGGI 900
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTrpAsnTrpLeuGlnSerLeuGly 298
QY 901 AAGTACTACGTTACGGTGTGAACCCATGGTCCAGCTCAAGGTGTGGTGTTCGCT 960
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
299 LysTrpTrpGlyTrpGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGGACACACTTCTACTAACCC 1020
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 336
QY 1021 ACTTTGGACTACTACCCAGCTACTTCCCATTTGAACGCTACTTTGTACGCTGACTCTCT 1080
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTrpValAspPheSer 358
QY 1081 CACGACAACTATGCTTCTTCTTCTGCTTTGGTTTGTACACGCTACTTAAGCCA 1140
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTrpAsnGlyThrGluPro 378
QY 1141 TTGCTACTACTCTGTTGAATCTATTGAAGAACTGACGGTACTCTGCTCTTGGACT 1200
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DB 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTrpSerAlaSerTrpVal 398
QY 1201 GTTCATTCTGCTCTAGAGCTTACGTTAGAAATGATGCAATGCAAGCTGAAAAGAACCA 1260
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
399 ValProPheGlyAlaArgAlaTrpPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1261 TTGGTTAGACTTTTGGTTAAGCAGACAGTGTTCCTATTCACGGTGTGCTTGCACAG 1320
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1321 TTGGGTAGATGTAAGAGACAGACTTCTGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGT 1380
DB   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY 1381 AACTGGGAAGAATGTTTCGCT 1401
DB 459 AsnTrpGlyGluCysPheSer 465
RESULT 8
US-09-044-718-78
: Sequence 78, Application US/09044718
: Patent No. 6391805
: GENERAL INFORMATION:
: APPLICANT: KOSTREMA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044.718
: CURRENT FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 78
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-09-044-718-78
Alignment Scores:
Pred. No.: 1,29e-176 Length: 465
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 4 Gaps: 2
US-09-488-265B-30 (1-1404) x US-09-044-718-78 (1-465)
QY 1 ATGGCGCTGTTTCGTCGCTACTGTCCATTGCCACCTTGTTCGGTTCACCAICCGGTACC 60
DB 1 MetValThrLeuThrPheLeuLeuSerAlaAlaLysLeuLeuSerGlyArgValSerAla 20
QY 61 GCCTTGGGTCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAAGT 120
DB 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTrpGlnCys 39
QY 121 TTCCAGAAATTTCTCACTTGTGGGTACATCTCTCCATTCCTCTCTTTCGGTGCAGCAA 180
DB 40 SerProAlaThrSerHisLeuTrpGlyGlnCysSerProPheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCAGACGTTCCAAAGGGTGTAGAGTACTTTCGTTCAAGTTTGTCT 240
DB 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACACGGTGTAGATACCCCAACTTCTCTGCGTCTAAGCGGTACTCTGCTTGTATTGAA 300
DB 80 ArgHisGlyAlaArgTrpProThrSerSerLysLysTrpLysLysLeuValThr 99
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301 GCTATTCAAGAACGCTACTGCTTCAAGGGTAAGTACGCTTCTTGAAGACTTACAAAC 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 AlaileGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

361 TACACTTTGGTGCTGACGACTTGACTCCATTTCGGTGAACAACAATGGTTAACTCTGCT 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

421 ATTAAGTTCTACAGAAGATACAGGCTTTGGCTAGAAAGATTGTTCCATTCATTACACT 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

481 TCTGGTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAACTCTCT 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 SerGlySerAspArgValIleAlaSerGlyGlyLysPheIleGluGlyPheGlnGlnAla 179

541 AAGTTGGCTGACCCAGTGCTAACCCACACAGCTTCTCCAGTTATTAAAGTTATTATT 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIlelle 198

601 CCAGAAGTGCTGGTTTCAACAACACTTTGGACCAAGGTTTGTGACTGCTTTCGAAGAA 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

661 TCTGAATTGGTCCACGAGCTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

721 GCTAGATTGGAAGCTCACTTGCAGGTGTTAACTTGACTGACGAGAGACTTGTAACTTG 780
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

781 ATGGACATGTCCTCCACTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 259 MetAspMetCysSerPheAspThrValAlaAla-gThrSerAspAlaSerGlnLeuSerPro 278

841 TTCTGTGACTTGTCTACTCACGAGAAATGGATTCAATACGACTACTTGAATCTTGGGT 900
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

901 AAGTACTACGGTTACGGTGCTGCTAACCCAGTTCAGCTTCAAGGTGTTGGTTTCTGCTT 960
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

961 AAGCAATTGATTGCTAGATTGACTACTCTCCAGTTCAAGACCACACTTCTACTAACCCAC 1020
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

1021 ACTTGGACTCTAACCCAGCTACTTTCCCATTTGAACGCTACTTGTACGCTGACTTCTCT 1080
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

1081 CAGCACAACTATGTTCTATTCTTCTCGCTTTCGGTTTGTACAAACGGTACTAAGCCA 1140
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

1141 TTGCTACTACTTCTGTGTAATCTATTGAAGAACTGACGGTTACTCTCTCTTCTGGACT 1200
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

1201 GTTCCATTCCGCTGCTAGAGCTTACGTTGAATGATGCAATGTGAAGCTGAAAGGAACCA 1260
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

1261 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCCATTTCACGGTTGCTGCTTTCACAG 1320
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Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

1321 TTGGGTAGATGTAAGAGACGACTTCTGTTGAAGGTTTCTTCTTCGCTAGACTCTGCTGT 1380
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
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Qy 1381 AACGGGAAGAATGTTTCGCT 1401
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 459 AsnTrpGlyGluCysPheSer 465

RESULT 9
US-09-636-499-6
; Sequence 6, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/09/636,499
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,960
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PKT
; ORGANISM: Aspergillus fumigatus
US-09-636-499-6

Alignment Scores:
Pred. No.: 1,29e-176 Length: 465
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 4 Gaps: 2

US-09-488-265B-30 (1-1404) x US-09-636-499-6 (1-465)
Qy 1 ATGGGGCTGTGGTGGTCTACTGCTCCATTCGACACCTGTCTGGTTCACATCCGGTACC 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy 61 GCCTTGGGTCTCGTGGTAACTCTCACTCTGTGACACTGTGTGACGGTGGTTACCAATGT 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2; AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy 121 TTCCCAAAATTTCTCACTTGTGGGTACATCTCTCCATCTCTCTCTCTCTCTCTCTCT 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59

Qy 181 TCTGCTATTTCTCCAGACGTTCCAAAGGTTGTAGAGT-ACITTCGTTCAAGTTTGTCT 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy 241 AGACACGGTCTAGATACCACTTCTTCTGCGCTCTAAGCGTACTCTGCTTGTATTGAA 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99

Qy 301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACTGCTTCTTGAAGACTTACAA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 AlaileGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

361 TACACTTTGGTGCTGACGACTTGACTCCATTTCGGTGAACAACAATGGTTAACTCTGCT 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

421 ATTAAGTTCTACAGAAGATACAGGCTTTGGCTAGAAAGATTGTTCCATTCATTACACT 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

481 TCTGGTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAACTCTCT 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 SerGlySerAspArgValIleAlaSerGlyGlyLysPheIleGluGlyPheGlnGlnAla 179

160 SerGlySerAspArgValIleAlaSerGlyGlyLysPheIleGluGlyPheGlnGlnAla 179
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 SerGlySerAspArgValIleAlaSerGlyGlyLysPheIleGluGlyPheGlnGlnAla 179
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Db 299 LysTyrTyGlyTyGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATGATTGCTAGATTGACTCCTCCAGTTCAAGACACACACTTCTACTAACCAC 2020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGGACTTAACCCAGCTACTTCCATTGACCTACTTGTACGGTGGACTTCTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyValAspPheSer 358
QY 1081 CAGGACACACTATGCTTCTATTTCTTCCTGCTTGGTTGTACACGGTACTAAGCCA 1340
Db 359 HisAspAsnMetValSerIlePheAlaLeuGlyLeuTyAsnGlyThrGluPro 378
QY 1141 TTGCTACTACTTCTGTTGAATCATATTGAAGAACTGACGGTACTTCTGCTTCTGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTySerAlaSerTrpVal 398
QY 1201 GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGTGAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyPheGlnThrMetGlnCysLysSerGluLysGluSer 418
QY 1261 TTGGTTAGAGTTTGGTTAAACACAGAGCTTCTCCATTGCACGGTGTGGTGTGACAA 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1321 TTGGGTAGATGTAAGAGAGACACTTCTGTTGAAGTTTGTCTTCCGCTAGATCTGGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY 1381 AACTGGGAAGATGTTTCGCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465
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RESULT 12

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US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 79
; LENGTH: 465
; TYPE: PR1
; ORGANISM: Aspergillus fumigatus
US-09-044-718-79
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Alignment Scores:

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Pred. No.: 9,86e-176 Length: 465
Score: 1879.00 Matches: 358
Percent Similarity: 84.15% Conservative: 35
Best Local Similarity: 76.66% Mismatches: 72
Query Match: 75.58% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265B-30 (1-1404) x US-09-044-718-79 (1-465)

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QY 1 ATGGGGGTGCTTCGTCGTGCTACTGTCCATTGCCACCTTTCGGTTCCACATCCGGTACC 60
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyLeuLeuSerGlyArgValSerAla 20
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QY 61 GCCTTGGCTCCTCGTGGTAACTCTCACTCTTGTGACACTGTGTGACGGTGGTACCAATGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyArgLysCys 39
QY 121 TTCACAGAAATTTCTCACTTGTGGGTGATACATCTCTCATCTCTCTCTTGGCTGACGAA 180
Db 40 SerProAlaIleThrHisLeuTrpGlyGlnTySerProPheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCAGAGCTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACACGGTGTAGATACCCAACTTCTCTCGCTCAAGCGGTACTCTGCTTGCATTGAA 300
Db 80 ArgHisGlyAlaArgTyProThrSerSerLysSerLysLysTyLysLysLeuValThr 99
QY 301 GCTATTCAAAAGACGCTACTGCTTTCAGGGTAAAGTACGGTTCTTTGAAGACTTACAAC 360
Db 100 AlalleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyAsn 119
QY 361 TACATTTGGTGTGTCAGACTTGACTCCATTCGGTGAACCAACAAATGGTTAACTCTGGT 420
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTTCTCAGAGATACAGAGCTTGGCTAGAAGATTGTTCGATTCATTAGAGCT 480
Db 140 IleLysPheTyGlnArgTyLysAlaLeuAlaArgSerValProPheIleArgAla 159
QY 481 TCTGTTCTCGACAGAGTATTGCTTCTCTCTGCTGAAAAGTTTCATTGAAGTTTCCAATGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179
QY 541 AAGTTGGTGCACCGAGTGTCTAACCCACACCAAGCTTCCAGTTATTAAGCTTATTATT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIle 198
QY 601 CCAGAAAGTGTGCTGGTTTACAACACACTTTGGACACCGGTTTGTGTTACTGCTTCCAGAA 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTCGGTGCAGACGCTTGAAGCTAACTCACTGCTGTTTTCGCTCCCAATTAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAAGCTCACTTGCAGGTGTAACTTGACTGACGACGAGCTGTGTAACCTG 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGGACATGTGCTCATTCGACACTGTTCGTAGAAGTCTGACGCTACTCAATTTGCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TCTCTGTGACTTGTTCACCTCAGCAGCAATGGATTCAATACGACTACTTCGCACTTGGGT 900
Db 279 PrecysGlnLeuPheThrHisAsnGlnTrpLysTyAsnTyLysLeuGlnSerLeuGly 298
QY 901 AAGTACTACGGTTACGGTGTGTAACCCATTGGCTCCAGCTCAAGGTGTTGGTTTCGT 960
Db 299 LysTyTyTyGlyTyGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATGATTGCTAGATTGACTCCTCCAGTTCAAGACACACACTTCTACTAACCAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGGACTTAACCCAGCTACTTTCGCTTGAAGCTACTTGTACGGTGGACTTCTCT 1080
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QY 1081 CAGGACACACTATGCTTCTATTTCTTCGCTTGGTTGTACACGGTACTAAGCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyAsnGlyThrGluGly 378
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QY 1141 TTGCTACTACTCTGTGTGTAATCTATGAAGAAACGACGGTACTCTCTCTCTCTGACT 1200
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RESULT 13
US-09-044-718-3
; Sequence 3, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREMA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044, 718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-3

Alignment Scores:
Pred. No. : 1,07e-175 Length: 439
Score: 1876.50 Matches: 351
Percent Similarity: 87.73% Conservatives: 35
Best Local Similarity: 79.77% Mismatches: 53
Query Match: 75.56% Indels: 1
DB: 4 Gaps: 1

US-09-488-265B-30 (1-1404) x US-09-044-718-3 (1-439)
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Db 21 TrpGlnTyTrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 40
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Db 161 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 179
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Db 180 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 199
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QY 682 GAAGCTAACTTCACCTGCTGTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTG 741
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QY 802 ACTGTTGCTAGAACTTCTGACGCTACTCAATTCCTCCATTCCTGCTGCTGCTGCTGCTGCT 861
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Db 240 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 259
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QY 862 GACCAATGGAATTCATACGACTACTTCCAAATCTTGGTAACTTACGTTACGTTACGGTGT 921
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Db 260 AsnGluTrpLysTyTrpAsnTyTrpLeuGlnSerLeuGlyLysTyTrpGlyTyGlyAla 279
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QY 922 GGTAAACCATTTGGTCCAGCTCAAGGTGTGTTGCTTAACCAATTTGATTGCTAGATTG 981
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Db 280 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuAlaArgLeu 299
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QY 982 ACTCACTCTCCAGTTCAAGACCACTTCTACTAACCAACACTTTGGACCTTACACCCAGCT 1041
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Db 300 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 319
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QY 1042 ACTTCCCATTTGACGCTACTTGTACGCTGCTCTCTCCAGCAGACACTATGTTCTTCT 1101
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Db 320 ThrPheProLeuAsnAlaThrMetTyTrpValAspPheSerHisAspAsnSerMetValSer 339
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QY 1102 ATTTTCTCGCTTTGGGTTTGTACACGGTACTAACGCCATTGCTACTACTCTCTGTGAA 1161
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QY 1162 TCTATTGAAGAACTGACGGTACTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221
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Db 360 SerAlaLysGluLeuAspGlyTyTrpSerAlaSerTrpValValProPheGlyAlaArgAla 379
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QY 1222 TACCTTGAATGATGCAATGTGAAGCTCAAAAGCAACCAATTCGTTAGAGTTTGGTTAAC 1281
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Db 380 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 399
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QY 1282 GACAGAGTTGTTCCATTCGACGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 1341
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Db 400 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 419
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QY 1342 GACTTCGTTGAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTTGGGAAGCAATCTTTCGCT 1401
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Db 420 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 439
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RESULT 14
US-09-044-718-12
; Sequence 12, Application US/09044718
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```
Patent No. 6391605
GENERAL INFORMATION:
APPLICANT: KOSTREMA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: van LOON, Adolphus
APPLICANT: VOGEL, Kurt
APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 449
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Alignment Scores:
Pred. No.: 1,08e-175 Length: 449
Score: 1878.50 Matches: 351
Percent Similarity: 87.73% Conservative: 35
Best Local Similarity: 79.77% Mismatches: 53
Query Match: 75.56% Indels: 1
Dbs: 4 Gaps: 1

US-09-488-265b-30 (1-1404) x US-09-044-718-12 (1-449)

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QY 142 TGGGTACATACCTCCATCTCTCTCTCTGCTGACCAATCTGCTATTCTCCAGAGCTT 201
DB 31 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 50
QY 202 CCAAGGGTGTAGAGTACTTCTGCTCAAGTTTGTCTAGACACGGTGTAGATACCCA 261
DB 51 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 70
QY 262 ACTTCTCTGCTGCTAAGCGCTACTCTGCTTTGATTGAAGCTATTTCAAAGACGGTACT 321
DB 71 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 90
QY 322 GCTTTCAGGGTAGTAGCTTCTTCTGAGACTTACACTTACACTTTGGTGGTGTGAGCAG 381
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QY 382 TTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGCTATTAGTTCTACAGAAGATAC 441
DB 111 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 130
QY 442 AAGCTTTGGGTAGAGAAGATTTCTCCATTCATTAGAGCTTCTGCTTCTGACAGAGTATT 501
DB 131 LysAlaLeuAlaArgSerValProPheIleArgAlaSerGlySerAspArgValIle 150
QY 502 CTTCTGCTGAGAAAGTTCATTGAGCTTCCAACTCTGCTAGTTGGTGGTCCAGCGTGTCT 561
DB 151 AlaSerGlyGlyLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 170
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DB 171 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 189
QY 622 AACACTTGGACCGAGTGTCTGACTGCTTCTGAGAGTCTTCAAGAGTCTGAGTGGTGGT 681
DB 190 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 209
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Db 210 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 229
QY 742 CCAGGTGTTAACTTGACTGACGAGAGAGCGTTGTTAACTTGATGACATGCTGTCACATTCGAC 801
DB 230 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 249
QY 802 ACTGTTGTTAGAACTTCTGACGCTACTCAATGTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 861
DB 250 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 269
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DB 270 AsnGluTyrLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrGlyTyrGlyAla 289
QY 922 GGTAAACCATTTGGTCCAGCTCAAGGTGTTGGTTTTCGTTAACGAATGATGCTAGATG 981
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DB 350 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 369
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QY 1282 GACAGAGTGTGCTTCCATTCGACGGTGTGCTGTTGCAAGTGGGTAGATGTTAAGAGAC 1341
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QY 1342 GACTTCGTTGAAGTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1401
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RESULT 15
US-09-044-718-81
Sequence 81, Application US/09044718
Patent No. 6391605
GENERAL INFORMATION:
APPLICANT: KOSTREMA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: van LOON, Adolphus
APPLICANT: VOGEL, Kurt
APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 81
LENGTH: 465
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-09-044-718-81

Alignment Scores:
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 08:05:37 ; Search time 70.6311 Seconds
(without alignments)
6289.894 Million cell updates/sec:

Title: US-09-488-265b-28

Perfect score: 2480

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 1175308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications_AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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3	1875	75.6	467	15	US-10-229-358-5	Sequence 5, Appli
4	1867	75.3	465	14	US-10-083-452-8	Sequence 8, Appli
5	1867	75.3	465	15	US-10-062-848-78	Sequence 78, Appl
6	1867	75.3	465	15	US-10-229-358-6	Sequence 6, Appli
7	1863	75.1	467	14	US-10-083-452-11	Sequence 11, Appl
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9	1860.5	75.0	467	9	US-09-929-060-3	Sequence 3, Appli
10	1859	75.0	465	15	US-10-062-848-80	Sequence 80, Appl
11	1858	74.9	465	15	US-10-062-848-79	Sequence 79, Appl
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13	1857.5	74.9	448	15	US-10-062-848-12	Sequence 12, Appl
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15	1851	74.6	462	15	US-10-229-358-12	Sequence 12, Appl
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23	1761	71.0	466	14	US-10-083-452-12	Sequence 12, Appl
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25	1719	69.3	466	14	US-10-083-452-13	Sequence 13, Appl
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27	1714	69.1	438	15	US-10-062-848-2	Sequence 2, Appli
28	1627	65.6	489	15	US-10-229-358-4	Sequence 4, Appli
29	1627	65.6	489	15	US-10-229-358-10	Sequence 10, Appl
30	1613	65.0	410	15	US-10-229-358-11	Sequence 11, Appl
31	1334	53.8	475	14	US-10-083-452-14	Sequence 14, Appl
32	1313.5	53.0	487	14	US-10-083-452-15	Sequence 15, Appl
33	1313.5	53.0	487	15	US-10-229-358-8	Sequence 8, Appli
34	1311	52.9	353	15	US-10-229-358-15	Sequence 15, Appl
35	1187	47.9	495	14	US-10-083-452-2	Sequence 2, Appli
36	1182	47.7	478	14	US-10-083-452-3	Sequence 3, Appli
37	902	36.4	284	15	US-10-229-358-19	Sequence 19, Appl
38	855	34.5	283	15	US-10-229-358-9	Sequence 9, Appli
39	855	34.5	283	15	US-10-229-358-24	Sequence 24, Appl
40	802.5	32.4	443	14	US-10-083-452-5	Sequence 5, Appli
41	798.5	32.2	439	14	US-10-083-452-7	Sequence 7, Appli
42	795.5	32.1	453	14	US-10-083-452-6	Sequence 6, Appli
43	781	31.5	442	14	US-10-083-452-4	Sequence 4, Appli
44	702.5	28.3	212	15	US-10-229-358-16	Sequence 16, Appl
45	401	16.2	312	15	US-10-229-358-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618 500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25

NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-10-083-452-9

Alignment Scores:
Pred. No.: 2,77e-198 Length: 467
Score: 2408.00 Matches: 457
Percent Similarity: 98.50% Conservative: 3
Best Local Similarity: 97.86% Mismatches: 7
Query Match: 97.10% Indels: 0
DB: 14 Gaps: 0

US-09-488-265B-28 (1-1404) x US-10-083-452-9 (1-467)

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QY 1 ATGGCGGTGTCGTCGCTACTCTCCATTCGCCACCTGTTCGGTCCACATCCGGTACC 60
DB 1 MetGlyValPheValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20
QY 61 GCCTTGGCTCTCTGCTGTAATTCCTACTCTGTGACACTCTTGACGGTGGTACCAATCT 120
DB 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValaspGlyGlyThrGlnCys 40
QY 121 TTCCAGAAATTTCTACTTTGGGTGGGTACTCTCCACTCTCTTCTGTCCTTTGGCAGACGAA 180
DB 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
QY 181 TCTGCTATTCTCCAGAGCTTCCAGAGCTGTAGAGTACTTCTGCTCAAGTTTGTCT 240
DB 61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80
QY 241 AGACACGGTGTAGATACCCCACTCTCTGCGTCTAAGCTTACTCTGCTGTGATGAA 300
DB 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGACGCTACTGCTTTCAAGGTAAAGTACGCTTCTTGAGAGCTTACAAC 360
DB 101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTTGGTGTGACGACTTGACTCCATTCGCTGAAAAACCAATGGTTAACTCTGCT 420
DB 121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140
QY 421 ATTAAGTTCTACAGAGATACAAGCTTTGGCTAGAAGATTGTTCCATTTCATAGACT 480
DB 141 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 160
QY 481 TCTGTTCTGACAGAGTTATTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 161 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180
QY 541 AGCTTGGCTGACCCAGCTTCTACACCAACCAAGCTTCTCAGTTATTACGTTGATCATT 600
DB 181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIle 200
QY 601 CCAGAAGGATCCGGTTACAAACACACTTTGGACCAACGCTACTGCTGCTGCTGCTGCTGCT 660
DB 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY 661 TCTGAATTAGTGACGAGCTTGAAGCTAACTTCTACTGCTTTGCTGCTGCTGCTGCTGCTGCT 720
DB 221 SerGluLeuGlyAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
QY 721 GCTAGATTGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
QY 781 ATGGACATGTGTCCATTCGACACTGCTGCTAGACTTCTGACGCTACTGATGCTGCTGCT 840
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DB 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
QY 841 TTCTGCTTTTGTCTACTCAGCAGCAATGGATCCCAATAGCACTACTTCGAAGCTTGGT 900
DB 281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300
QY 901 AAGTACTACGGTTACGGTGTGTAACCCATTCGGTCCAGCTCAAGGTGTGGTTCGCT 960
DB 301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320
QY 961 AACGAATGATTGCTAGATTGACTCTCTCCAGTTCACAGACACACTTCTACTAACAC 1020
DB 321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340
QY 1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTCACCGCTACTTTGCTGCTGCTGCTGCT 1080
DB 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360
QY 1081 CACGACAACTATGATATCTATTTCTTCTGCTTGGCTTGTACACCGTACCAGCCA 1140
DB 361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380
QY 1141 TTGCTACTTCTGCTGTAATCTATTTGAAGAACTGACGGTACTCTGCTTCTTGGACT 1200
DB 381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400
QY 1201 GTTCATCTGCTGCTAGAGCTTACGTTGAATGATGATGATGATGATGATGATGATGATGAT 1260
DB 401 ValProPheGlyAlaArgAlaTyrValGluMetGlnCysGlnAlaGluLysGluPro 420
QY 1261 TTGCTGAGAGTTTGGTTAACGACAGAGTTGTTCCATTCACCGTGTGCTGTTGACAAG 1320
DB 421 LeuValArgValLeuValAlaAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440
QY 1321 TTGGGTAGATGTAAGAGAGAGACTTGGTTGAAGGTGTGTTGAGAGTTGCTTCTGCTGCTGCT 1380
DB 441 LeuGlyArgCysLysArgAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGCTGAATGTTTCGCT 1401
DB 461 AsnTrpAlaGluCysPheAla 467
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RESULT 2

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US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seilen
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
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/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/233,510
/ FILING DATE: 20-JAN-1999
/ APPLICATION NUMBER: 07/688,578
/ FILING DATE: 24-MAY-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Murashige, Kate H.
/ REGISTRATION NUMBER: 29,954
/ REFERENCE/DOCKET NUMBER: 24615-20026.00
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-327-7250
/ TELEFAX: 415-327-2951
/ INFORMATION FOR SEQ ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 467 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-10-079-709-32

Alignment Scores:
Pred. No.: 1,84e-152 Length: 467
Score: 1875.00 Matches: 353
Percent Similarity: 84.37% Conservative: 43
Best Local Similarity: 75.59% Mismatches: 73
Query Match: 15 Indels: 0
DB: 15 Gaps: 0

US-09-488-265B-28 (1-1404) x US-10-079-709-32 (1-467)

QY 1 ATGGCGGTTCGTCGCTACTGTCATGCCACCTGTGTCGTTCCACATCCGATACC 60
DB 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuSerGlyValThrSerGlyLeu 20
QY 61 GCCTTGGGTCCGCGGGTAATTCACCTCTTGTGACACTGTGACGGTGTACCAATGI 120
DB 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TTCACAGAAATTCACATTTGGGGTACTACTCTCCACTCTCTTGGGAGAGAA 180
DB 41 PheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
QY 181 TCCTGCTATTCACAGAGCTTCCACAGCACTGTAGACTTTCGTCAGGTTTGTCT 240
DB 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY 241 ACACAGGTGCTAGATACCAACTCTCTTCGGCTAAGGCTTACTCTGCTTGTGAA 300
DB 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGACGCTACTCTCTTCAAGGTAGTACGCTTCTTGAAGACTTACAAC 360
DB 101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTGGGTGCTGACAGCTTACTCCATTCGTCGGTGAACCAACCAAGTTACTCTGT 420
DB 121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAGTCTCAGACAGATACAGGCTTGGCTAGAAAGATGTTCATTCATTAAGACT 480
DB 141 IleLysPheTyrGlnArgTyrGlnSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 481 TCTGGTCTCAGACAGTTATTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180
QY 541 AAGTTGGCTGACCCAGGTCTCAACCAACCAACCAACCAACCAACCAACCAACCAAC 600
DB 181 LysLeuLysProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200
QY 601 CCAGAGGATCCGGTTACAAACAACTTTGGACCACTTGTGACCTGCTTGTGACCAAC 660
DB 601 LysLeuLysProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200
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DB 201 SerGluAlaSerSerSerAsnThrLeuAspProGlyThrCystThrValPheGluAsp 220
QY 661 TCTGAATTAGGTGACGAGCTTGAAGCTTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 721 GCTAGATTGAAGCTGACCTTCCAGGCTTACTTGTAGCTGACGAGAGAGCTTGTACTTG 780
DB 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
QY 781 ATGGACATGTGTCCTCAGACTTCGCTAGCACTTCGCTAGCACTTCGCTAGCACTTCGCT 840
DB 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
QY 841 TTCTGTGCTTGTTCCTCAGCAAGATGGAATCCAAATACGACTTCTGCAAGCTTGGGT 900
DB 281 PheCysAspLeuPheThrHisAspGlnTrpIleAsnIleAspTyrLeuGlnSerLeuLys 300
QY 901 AAGTACTAGGTTACGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY 961 AACGAATTGATGCTAGATTGACTCTCCACTCTCCAGTTCAGACCACTTCTACTAACCCAC 1020
DB 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCCAATGAAGCTACTTTGTACGCTGACTTCTCT 1080
DB 341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
QY 1081 CAGCAACACACTATGATATCTATTTCTGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1140
DB 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrIlePro 380
QY 1141 TTGCTTACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyrPhe 400
QY 1201 GTTCCATTCGCTGCTAGACTTACGTTGNAATGATGCAATGCTCAAGCTGAAAGAACCA 1260
DB 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnPro 420
QY 1261 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTTCCATTGCTGCTGCTGCTGCTGCTGCT 1320
DB 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
QY 1321 TTGGGTAGATGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGCTCAATGTTTGGCT 1401
DB 461 AspTyrAlaGluCysPheAla 467

RESULT 3
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating San
; FILE REFERENCE: GC596-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
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TYPE: PRT
ORGANISM: Aspergillus niger
US-10-229-358-5

Alignment Scores:

Pred. No.: 1.84e-152 Length: 467
Score: 1875.00 Matches: 353
Percent Similarity: 84.37% Conservative: 41
Best Local Similarity: 75.59% Mismatches: 73
Query Match: 75.60% Indels: 0
DB: 15 Gaps: 0

US-09-488-265b-28 (1-1404) x US-10-229-358-5 (1-467)

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Qy 1 ATGGCGTGTTCGTCGGTACTGTCCATTCGCCACTTGTTCGGTCCACATCCGGTACC 50
Db 1 MetGlyValSerAlaValLeuLeuProLeuLeuSerGlyValThrSerGlyLeu 20
Qy 61 GCCTTGGTCTCTGCTGTAATTCCTACTCTGTGCACACTGCTTCACGGTGGTACCAATCT 120
Db 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyThrGlnCys 40
Qy 121 TTCACAGAAATTCCTACTCTGTGGGTACTCTCCACTCTCTCTTGTGGCAGACGAA 180
Db 41 PheSerGluThrSerHisLeuTyrGlyGlnThrAlaProPhePheSerLeuAlaAsnGlu 60
Qy 181 TCTGCTATTCTCCAGAGCTCCAGACGACTGTAGAGTCACTTCTCCAGTTTGTCT 240
Db 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
Qy 241 AGACACGGTGTAGATACCCCACTTCTCTCGGCTCTAAGCTTACTCTGCTTTGATGAA 300
Db 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuLeuGlu 100
Qy 301 GCTATTCAAAAGACGCTACTGCTTTCACGGTAAAGTACGCTTCTTGAAGACTTACAC 360
Db 101 GluIleGlnGlnAsnAlaThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
Qy 361 TACACTTGGTGTGTCGACTTCACTCCATTCGGTGAACCAACCAATGGTTAACTCTGT 420
Db 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
Qy 421 ATTAGTCTCACAAGATACAGGCTTTCGGTAGAAGATGTTCATTCATTAAGCT 480
Db 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
Qy 481 TCTGCTTCTGACAGAGTATTGCTTCTGCTGAAAAGTTTCATTAAGGTTTCCCAATCTGT 540
Db 161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180
Qy 541 AAGTTGGTGCACAGGCTTCAACACACAGCTTCTCCAGTTATTACGTGATCAT 600
Db 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle 200
Qy 601 CCAGAAGATCCGGTTACAAACACACTTGGACACCGTACTTGTACTGTTTCGGAAGAC 660
Db 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
Qy 661 TCTGAATTAGGTGACGAGGTTGAGAGCTTAACCTTCACTGTTTGTTCGCTCAGCTATTAGA 720
Db 221 SerGluLeuAlaAspThrValIleGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
Qy 721 GCTAGATTGGAGCTGCTCCAGGCTTCACTTGTACTGTCAGACGAGCTGTTTACTTG 780
Db 241 GlnArgLeuGlnAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrThrLeu 260
Qy 781 ATGGACATGTGTCCATTCGACACTGTCCGCTAGAACCTTCTGACGCTACTGAATTCCTCCA 840
Db 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
Qy 841 TTCTGTGCTTGTTCACATCAGCAGCAATGGATCCAAATACGACTACTTCCAAAGCTTGGGT 900
Db 281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

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Qy 901 AAGTACTACGTTTACGGTCTGTGTAAACCCACTGGGTCCAGCTCAAGGTSITGGTTTCCT 960
Db 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
Qy 961 AAGCAATGATTCGTAGTACTCTCTCCACTCTCCAGTTTCAAGACACACTTCTACTAACAC 1020
Db 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340
Qy 1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATCTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db 341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
Qy 1081 CAGCAACACTATGATATCTATTCTTCGCTTTCGGTTTGTATACACGGTACCAGCCA 1140
Db 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
Qy 1141 TTGCTACTACTCTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTCTCTTGGGACT 1200
Db 381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaThrThr 400
Qy 1201 GTTCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCACAGCTGAAAGAACCA 1260
Db 401 ValProPheAlaSerArgLeuTyrValGluMetCysGlnAlaGluGlnGluPro 420
Qy 1261 TGTGTTAGAGTTTGGTTAACGACAGAGTTGTTCCATTCACGGTGTGCTGTTGACAA 1320
Db 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
Qy 1321 TTGGGTAGATGTAAAGACAGACGCTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGT 1380
Db 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
Qy 1381 AACTCGGCTCAATCTTTCGCT 1401
Db 461 AspTrpAlaGluCysPheAla 467

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RESULT 4

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US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618,500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/050,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-083-452-8

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Alignment Scores: 8.97e-152 Length: 465
Pred. No.: 1867.00 Matches: 355
Score: 83.73% Conservative: 36
Percent Similarity:

QY	121	TTCCAGAAATTTCTC	ACTTGTGGGTACCT	ACTCTCCATACCTTCTCTTTGGCAGACGAA	180
DB	40	SerProAlaThrSerHisLeu	TrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu	59	
QY	181	TCGCTATTTC	CCAGAGCTTCAGACGACTCTAGAGTTAC	TTTCGTTCAAGTTTGTCT	240
DB	60	LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer	79		
QY	241	AGACAGGTGCTAGATACCAACTTCTTTCGCTTAAGGCTTACTCTGCTTGTGAATGAA	300		
DB	80	ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr	99		
QY	301	GCTATTCAAAAGACGCTACTGCTTTCAAGGTAAGTACGCTTTCTTGAAGACTTACAAC	360		
DB	100	AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn	119		
QY	361	TACACTTTGGTGTGACGACTTGACTCCATTCGGTGAAGCAACCAATGGTTACTCTGGT	420		
DB	120	TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGlnGlnLeuValAsnSerGly	139		
QY	421	ATTAAGTTCTACAGAAGATACAGGCTTTGGCTAGAAAGATTGTCATTCATTACAGCT	480		
DB	140	IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleAlaGln	159		
QY	481	TCGTGGTCTGACAGAGTTATGCTTCGTGTGAAGTTTCATTTGAAGTTTCCAACTGCT	540		
DB	160	SerGlySerAspArgValIleAlaSerGlyGlnLysPheIleGluGlyPheGlnGlnAla	179		
QY	541	AAGTTGCTCACCACAGGTTCTCAACACACACAGCTTCTCCACTTATTACGTTGATCAIT	600		
DB	180	LysLeuAlaAspProGlyAla	198		
QY	601	CCAGAGGATCCGGTTACACACACACTTTGGACACAGGTACTTGTACTGCTTTCGAAGAC	660		
DB	199	ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGlnAla	218		
QY	661	TCGTAAATTAGTGACGACGTTGAAGCTTAACCTTCACCTGCTTTGTTCGCTCCAGCTATTAGA	720		
DB	219	SerGlnLeuGlyAspGluAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg	238		
QY	721	GCTAGATTGGAAGCTGACTTCCAGGTTGTACTTTGACTCAGCAAGACGTTGTTTACTTG	780		
DB	239	AlaArgAlaGlnLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu	258		
QY	781	ATGGACATGTGCTCCATTCGACACTGCTCGCTAGAACTTCTCACGCTACTGAATGTCTCCA	840		
DB	259	MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro	278		
QY	841	TTCTGTGCTTTGTTCTACGACGAAATGATCCAAATACGACTACTTGCAAAGCTTGGGT	900		
DB	279	PheCysGlnLeuPheThrHisAsnGlnTrpLysLysTyrAsnTyrLeuGlnSerLeuGly	298		
QY	901	AAGTACTACGTTACGGTGTGTTAAACCATTCGGTCCAGCTCAAGGTGTGTTGCTGCT	960		
DB	299	LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr	318		
QY	961	AACGAATTGATTGTAGATTGACTCTCTCCAGTTCAAGACACACTTCTACTAAGCAC	1020		
DB	319	AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer	338		
QY	1021	ACTTTGACACTTACCCAGCTACTTCCCATTTGAACGCTACTTGTACGCTGACTTCTCT	1080		
DB	339	ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer	358		
QY	1081	CACGACACACTATGATATCTATTTCTTCGCTTTGGTTTGTACAACGGTACCAAGCCA	1140		
DB	359	HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro	378		
QY	1141	TTGTCTACTACTTCTGTGTAATCTATTGAAGAACTCAGGTTTACTCTGCTTCTTGACT	1200		
DB	379	LeuSerArgThrSerValGluSerAlaLysGlnLeuAspGlyTyrSerAlaSerTrpVal	398		

```

Qy 1201 GTTCCATTCCGCTAGAGCTTACGTTGAATATGATGCAATGTCACAGTCGAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaIatYrPheGluThrMetGlnCysLysSerGluLysGluPro 418
Qy 1261 TTGGTTAGAGCTTTGGTTAACGACACAGAGTGTTCCTCAATTGCACGGTTGCTGCTGTGACAAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValaIProleuHisGlyCysaspValAspLys 436
Qy 1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGGAAGGTTTGTCTTCGCTAGATCTGGTGGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
Qy 1381 AACTGGCTGAATGTTTCGCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465

RESULT 6
US-10-229-358-6
; Sequence 6, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-229-358-6

Alignment Scores:
Pred. NO.: 8.97e-152 .Length: 465
Score: 1867.00 Matches: 355
Percent Similarity: 83.73% Conservative: 36
Best Local Similarity: 76.02% Mismatches: 74
Query Match: 75.28% Indels: 2
Db: 15 Gaps: 2

US-09-488-265B-28 (1-1404) x US-10-229-358-6 (1-465)

```

```
QY 361 TACACITTTGGTGTGCTACGACACTTACCTCCATTCGGTGAAACCAAGGTTAACTCTGGT 420
Db 120 TyrThrLeuGlyAlaAspSerLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTTCTACAGAAGATTAAGGCTTTGGCTAGAAAGATTTCTCCATTCATTAAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValProPheIleArgAla 159
QY 481 TCTGGTTCTACAGAGATTATGCTTCGTCGAAAGTTCATTAAGGTTTCCAACTCTGT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlnGlnAla 179
QY 541 AAGTTGGCTGACCAGGTTCTCAACCAACCAAGCTTCTCAGTTATTAACGTGATCAIT 600
Db 180 LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAAGATCCGGTTACAAACACACTTTGGACACAGGTACTTGTACTGCTTTCGAAGAC 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTAGGTGACGAGCTGAAGCTAACTTCTCAGCTCTTGTTCGCTCCAGCTATTAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGAAGCTGACITGCCAGGTGTACTTTGACTGACGACGACGCTGTGTACTTIG 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGGACATGTGTCATTCGACACTGTGCTAGAACCTTCTGACGCTACTGAATTTGTCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCGTGCTTTGTCACATCAGCAGGAATGATGATCAATACGACTACTTCGAAAACCTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluThrLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGGTTACGGTGTGCTGCTAAACCTTTGGGTCAGCTCAAGGIGTGTGCTCGCT 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATTGATTGCTAGATTGACTCCTCTCCAGTTCACAGCACACTTCTATACACCAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGACACTATACCCAGCTACTTCTCCATTTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CACGACAACTATGATATCTATTTCTTCGCTTTGGGTTGTACACGCTACCAAGCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY 1141 TTGCTACTACTTCTGTTGAATCTATTGAAGAACTACGCTTACTTCTGCTTCTTGGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY 1201 GTTCCATTCGCTAGAGCTTACGTGGAATGATCAATGTCAAGCTGAAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1261 TTGTTTAGAGTTTGGTTAAACGACAGAGTTGTTCATTCGACGGTTGTGCTGTTGACAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1321 TGGGTAGATCATAGACAGACGACTTCTGTTCAAGGTTTGTCTTCGCTAGATCTGTTGGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY 1381 AACTGGGCTGAATGTTTCGCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465
```

RESULT 7

```
US-10-083-452-11
: Sequence ID, Application US/10083452
: Publication No. JS20020127218A1
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618.500-US
: CURRENT APPLICATION NUMBER: US/10/083,452
: PRIOR FILING DATE: 2002-02-26
: PRIOR APPLICATION NUMBER: US/09/273,871
: PRIOR FILING DATE: 1999-03-22
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: PRIOR FILING DATE: 1998-06-25
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11
: LENGTH: 467
: TYPE: PRT
: ORGANISM: Aspergillus ficuum
US-10-083-452-11

Alignment Scores:
Pred. No.: 1,98e-151 Length: 467
Score: 1863.00 Matches: 351
Percent Similarity: 83.94% Conservative: 41
Best Local Similarity: 75.11% Mismatches: 75
Query Match: 75.12% Indels: 0
DB: 14 Gaps: 0

US-09-488-265b-28 (1-1404) x US-10-083-452-11 (1-467)
QY 1 ATGGGGGTGCTGCTGCTGCTACTGCTCCATTCGACCACTTGTTCGGTTCCACATCCGGTACC 60
Db 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20
QY 61 GCCTTGGGCTCTCGTGGTAATTCTCCTCTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TTCCCAAGAAATTTCTCAGCTTGGGGTACTACTCTCCATCTTCTTTCGACAGCA 180
Db 41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
QY 181 TGTGCAATTTCTCCAGACGCTTCCAGACGACTAGTAGTACTTTCGTTCAAGTTTGTCT 240
Db 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY 241 ACAGACGGTGTAGATACCAACTTCTCTCGGCTCTAAGGCTTACTGCTGCTTGTGATTGAA 300
Db 81 ArgHisGlyValArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
QY 301 GCTATTTCAAAGAAAGCTACTGCTTCAAGGGTAAAGTACGCTTCTTGAAGACTTTACAAC 360
Db 101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTTGGTGTGACGACTTGACTCCATTCGTTCCGTTGAAACCAATGGTTAACTCTGGT 420
Db 121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAAGTTCTACAGAGATACAAAGCTTTGGCTAGAAAGTTCATTAAGTTCATTAGACT 480
Db 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
```

```
481 TCTGGTTCACAGAGTATTCCTCTCTGCTGAAAGTTCATTGAAGGTTTCCAACTCCT 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheIleSerThr 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
541 AAGTTGGCTGACCCAGGTTCTCAACACACACCAAGTCTCCAGTTATTAAAGTGATCAT 600
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 LysLeuLysAspProArgAlaGlnProGlyGlnSerProLysIleAspValIle 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
601 CCAGAAGGATCCGGTTACACACACACTTTGGACACAGCTACTTGTACTGCTTTTGAAGAC 660
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
661 TCTGAATAGGTCAGCAGCTTGAAGCTTAACCTCACTTCTGCTTCTCCAGCTATTAGA 720
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaIlePheValProSerIleArg 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
721 GCTAGATGGAAGCTGACTTGCAGGTGTTACTTTGACTGACGAAGAGCTTGTATTATG 780
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrThrLeu 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
781 ATGGACATGTCCTTCCACACTGTCGCTAGAACTTCTGACGCTACTGAATTCCTCCA 840
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
261 MetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSerPro 280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAAATACGACTACTTGCAAAGCTTGGT 900
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
901 AAGTACTAGGTTACGGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 960
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
961 AACGAATGATTGCTAGATTGACTCCTCTCCAGTTTCAAGACCACTTCTACTAACCAAC 1020
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerAsnHis 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1021 ACTTTGGACTCTAACCCAGCTACTTCCATTGAACGCTACTTTGTACGCTGACTCTCT 1080
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
341 ThrLeuAspSerSerProAlaThrPheProLeuLysSerThrLeuTyrAlaAspPheSer 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1081 CACGACAACTATGATATCTATTCTTCGCTTGGGTTTGTCAACGGTACCAAGCCA 1140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1141 TTGCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTACTTCTGCTTCTGACT 1200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 LeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaIleThr 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAATGATGCAATGTCAGCTGAAAGGACCA 1260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGlnAlaPro 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1261 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCATTGACGGTGTGCTGTTGACAAAG 1320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1321 TTGGGTAGATGTAAGAGACACACTTCTGTTGAAGCTTGTCTTTCGCTAGATCTGCTGT 1380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1381 AACTGGGCTGAATGTTTCGCT 1401
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
461 AspTyrAlaGluCysPheAla 467
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 8

```
US-10-213-990-24
: Sequence 24, Application US/10213990
: Publication No. US20030082595A1
: GENERAL INFORMATION:
: APPLICANT: Jiang, Ro
: APPLICANT: Bussey, Howard
: APPLICANT: Storms, Reg
: APPLICANT: Roemer, Terry
```

```
: TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
: TITLE OF INVENTION: ENZYMES AND METHODS OF USE
: FILE REFERENCE: 10182-019-999
: CURRENT APPLICATION NUMBER: US/10/213,990
: CURRENT FILING DATE: 2002-08-05
: NUMBER OF SEQ ID NOS: 72
: SCFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24
: LENGTH: 474
: TYPE: PRT
: ORGANISM: Aspergillus
: US-10-213-990-24
Alignment Scores:
Pred. No.: 3 27e-151 Length: 474
Score: 1860.50 Matches: 351
Percent Similarity: 84.12% Conservative: 41
Best Local Similarity: 75.32% Mismatches: 67
Query Match: 75.02% Indels: 7
Gaps: 2
Db: 15
```

US-09-488-265b-28 (1-1404) x US-10-213-990-24 (1-474)

```
Qy 4 GCGGTGTTCTGCTGCTACTGTCATGCCACCTTGTTCGGTTCCACATCCGGTACCGCC 63
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16 GlyAlaValValLeuIleLeuLysArgSerArgValSerAlaAlaProSerSer 33
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 64 TGGGTCTCTGGTAAATTCCTACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTC 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34 -----AlaGlySerLysSerCysAspThrValAspLeuGlyTyrGlnCysSer 49
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 124 CCAGAAATTTCTCCTGTGGGTACTACTCTCTCACTCTCTTCTTGGACACGAATCT 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 50 ProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGluLeu 69
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 184 GCTATTCTCCACAGCTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTGTCTAGA 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 70 SerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSerArg 89
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 244 CACGGTGTCTAGATACCAACTTCTCTGCTGCTTCTAAGCTTACTCTCTTGTGATGAAGCT 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 90 HisGlyAlaArgTyrProThrSerSerLysSerLysLysLysLysLysLysValThrAla 109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 304 ATTCAAAGAACGCTACTGCTTTCAAGGTAAGTACGCTTCTTGAAGACTTACAACTAC 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110 IleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyr 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 364 ACTTTGGGTCTCACCACCTGACTCCATTCGTTGAAACCAATGTTTAACTCTGTTATT 423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130 ThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIle 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 424 AAGTTCTACAGAAGATACAGGCTTTGGCTAGAAGAAATTTCCATTTCATTAGAAGCTTCT 483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 150 LysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAlaSer 169
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 484 GGTCTCAGACAGTTATTGCTCTGCTGAAAGTTCATTGAAGGTTTCCAACTCCTAAG 543
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 GlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAlaLys 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 544 TTGGCTGACCCAGGTTCTCAACCCACCAAGCTTCTCCAGTTATTAACTGAATCATTCCTCA 603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 190 LeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIlePro 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 604 GAAGGATCCGGTTTACAAACACACTTTGGACCCAGGTTACTTGTACTGCTTTCGAAGACTCT 663
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 209 GluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAlaSer 228
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 664 GAATTAGGTGACCACTTCAAGCTTCACTGCTTGTCTGCTCCACCTTATTAGACT 723
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 229 GlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAla 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 724 AGATTGGAAGCTGACTTGCAGGTGTTACTTTCAGTACGACGAAGCTTCTTACTTGTATG 783
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: October 3, 2003, 07:48:21 ; Search time 21.9567 Seconds
(without alignments)
5642.336 Million cell updates/sec

Title: US-09-488-265B-30
Perfect score: 2486
Sequence: 1 atggggcgtgttcgtcgtct.....gggaagaatttcgtcttaa 1404

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues
Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_n2p.model -DEV=xlp
-O=/cgn2.1/USPTO_spool/US09488265/runat_03102003_074813_12239/app_query.fasta_1.4693
-DB=Issued_Patents_AA -QMI=fastan -SUFFIX=oct3.ra -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09488265.ecgn.1.1.99 -runat_03102003_074813_12239 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -BARN_TIMEOUT=30 -THREAS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
Issued_Patents_AA:*
1: /cgn2.6/ptodata/1/iaa/5A.COMB.pcp.*
2: /cgn2.6/ptodata/1/iaa/5B.COMB.pcp.*
3: /cgn2.6/ptodata/1/iaa/6A.COMB.pcp.*
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5: /cgn2.6/ptodata/1/iaa/PCBUS.COMB.pcp.*
6: /cgn2.6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2308	92.8	467	4	US-09-273-871A-9
2	2182	87.8	441	3	US-09-121-425-1
3	2182	87.8	441	3	US-09-634-493A-1
4	2170	87.3	467	3	US-09-121-425-2
5	2170	87.3	467	4	US-09-634-493A-2
6	1888	75.9	465	3	US-08-868-435-33
7	1888	75.9	465	4	US-08-744-231-33
8	1888	75.9	465	4	US-09-044-718-78
9	1888	75.9	465	4	US-09-636-499-6
10	1888	75.9	465	4	US-09-273-871A-8
11	1880	75.6	465	4	US-09-044-718-80
12	1879	75.6	465	4	US-09-044-718-79

13	1678.5	75.6	439	4	US-09-044-718-3	Sequence 3, Appli
14	1878.5	75.6	449	4	US-09-044-718-12	Sequence 12, Appl
15	1876	75.5	465	4	US-09-044-718-81	Sequence 81, Appl
16	1854	74.6	469	4	US-09-044-718-82	Sequence 82, Appl
17	1852	74.5	467	1	US-07-923-724-8	Sequence 8, Appli
18	1852	74.5	467	2	US-06-609-426A-8	Sequence 8, Appli
19	1852	74.5	467	2	US-08-374-652C-2	Sequence 2, Appli
20	1848	74.3	467	1	US-08-151-574-32	Sequence 32, Appl
21	1848	74.3	467	1	US-08-146-424-20	Sequence 20, Appl
22	1848	74.3	467	1	US-08-693-709-2	Sequence 2, Appli
23	1848	74.3	467	2	US-08-419-448-32	Sequence 32, Appl
24	1848	74.3	467	2	US-08-819-825-3	Sequence 3, Appli
25	1848	74.3	467	3	US-09-163-642-3	Sequence 3, Appli
26	1848	74.3	467	4	US-09-233-510-32	Sequence 32, Appl
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30	1841	74.1	467	4	US-09-929-060-3	Sequence 3, Appli
31	1836	73.9	467	4	US-09-273-871A-11	Sequence 11, Appl
32	1829	73.6	462	4	US-09-636-499-12	Sequence 12, Appl
33	1822	73.3	466	3	US-08-868-435-35	Sequence 35, Appl
34	1822	73.3	466	4	US-08-744-231-35	Sequence 35, Appl
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36	1819	73.2	466	4	US-08-744-231-12	Sequence 12, Appl
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39	1804.5	72.6	463	4	US-08-744-231-29	Sequence 29, Appl
40	1804.5	72.6	463	4	US-09-273-871A-10	Sequence 10, Appl
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44	1794	72.2	443	3	US-09-155-855-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1

US-09-273-871A-9
? Sequence 9, Application US/09273871A
? Patent No. 6514495
? GENERAL INFORMATION:
? APPLICANT: Svendsen, Allan;
? TITLE OF INVENTION: Phytase Variants
? FILE REFERENCE: 5618 500-US
? CURRENT APPLICATION NUMBER: US/09/273, 871A
? CURRENT FILING DATE: 1999-03-22
? PRIOR APPLICATION NUMBER: PA 1998 00407
? PRIOR FILING DATE: 1998-03-23
? PRIOR APPLICATION NUMBER: PA 1998 00806
? PRIOR FILING DATE: 1998-06-19
? PRIOR APPLICATION NUMBER: PA 1998 01176
? PRIOR FILING DATE: 1998-09-18
? PRIOR APPLICATION NUMBER: PA 1999 00091
? PRIOR FILING DATE: 1999-01-22
? PRIOR APPLICATION NUMBER: 60/080,129
? PRIOR FILING DATE: 1998-03-31
? PRIOR APPLICATION NUMBER: 60/090,675
? PRIOR FILING DATE: 1998-06-25
? NUMBER OF SEQ ID NOS: 15
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 9
? LENGTH: 467
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Variation
US-09-273-871A-9
Alignment Scores:
Pred. No.: 7.66e-218 Length: 467
Score: 2308.00 Matches: 436
Percent Similarity: 95.72% Conservative: 11

Best Local Similarity: 93.36% Mismatches: 20
Query Match: 92.84% Indels: 0
DB: 4 Gaps: 0

US-09-488-265B-30 (1-1404) x US-09-273-871A-9 (1-467)

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DB 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTy-GluCys 40
QY 121 TTCGAGAAATTTCTCACTTGGGGTACATACCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 41 PheProGluIleSerHisLeuIrpGlyGlnTySerProTyPheSerLeuGluAspGlu 60
QY 181 TCTGCTATTCTCCAGACGTTCCAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
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DB 81 ArgHisGlyAlaArgTyrProThrSerSerLysAlaTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGAAGCTACTGCTTCAGGGTAAAGTACGCTTCTTGAAGACTTACAAAC 360
DB 101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTGGGTGCTGACAGCTTACTCCATTCGTTGAGAACAAAGTTAACTCTGGT 420
DB 121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140
QY 421 ATTAAGTCTACAGAGATACAAAGCTTGGCTAGAAAGATTGTTCCATTCAITAGACT 480
DB 141 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 160
QY 481 TCTGGTCTGACAGAGTTATTGCTCTGCTGAAAAGTTCAATGAAGGTTTCCAATCTGCT 540
DB 161 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180
QY 541 AAGTTGGCTGACCCAGGCTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATT 600
DB 181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIleIle 200
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RESULT 2

US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418

GENERAL INFORMATION:

; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112668.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

; LENGTH: 441

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: consensus

; OTHER INFORMATION: sequence

US-09-121-425-1

Alignment Scores:
Pred. No.: 1,73e-205 Length: 441
Score: 2182.00 Matches: 410
Percent Similarity: 95.46% Conservative: 11
Best Local Similarity: 92.97% Mismatches: 20
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DB: 3 Gaps: 0

US-09-488-265B-30 (1-1404) x US-09-121-425-1 (1-441)

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QY 199 GTTCCAAAGGGTCTAGAGTTACTTCTGTTCAAGTTTGTCTAGACACGGTGTAGATAC 258
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441 Ala 441
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US-09-634-493A-1
: Sequence 1, Application US/09634493A
: Patent No. 6579975
: GENERAL INFORMATION:
: APPLICANT: Lehmann, Martin
: TITLE OF INVENTION: Consensus Phytases
: FILE REFERENCE: consensus Phytases 13239
: CURRENT APPLICATION NUMBER: US/09/634,493A
: CURRENT FILING DATE: 2000-08-08
: PRIOR APPLICATION NUMBER: US/09/121,425
: PRIOR FILING DATE: 1998-07-23
: PRIOR APPLICATION NUMBER: EPO 97112688.3
: PRIOR FILING DATE: 1997-07-24
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 1
: LENGTH: 441
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: consensus
: OTHER INFORMATION: sequence
US-09-634-493A-1
Alignment Scores:
Pred. No.: 1,73e-205 Length: 441
Score: 2182.00 Matches: 410
Percent Similarity: 95.46% Conservative: 11
Best Local Similarity: 92.97% Mismatches: 20
Query Match: 87.77% Indels: 0
DB: Gaps: 4
US-09-488-265b-30 (1-1404) x US-09-634-493A-1 (1-441)
QY 79 AACCTCTCACTCTGTGCACACTGTTGACGCTGGTACCATTGTTCCCAAAAATTTCTCAC 138
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGluIleSerHis 20
QY 139 TTGTGGGGTACATCTCTCCATCTCTCTCTTGGGTGACGAATCTGCTATTTCTCAGAC 198
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21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40
QY 199 GTTCCAAAGGGTTGTAGAGTTACTTTCGTTTCAAGTTTGTCTAGACACGGTGTGATAC 258
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41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr 60
QY 259 CCAACTCTCTCGGCTCAAGCGTACTCTGCTTTGATTGAAGCTATTCAAAGAAGCGCT 318
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61 ProThrSerSerLysSerCysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla 80
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QY 439 TACAAGCCTTGGCTAGAAAGATTGTCATTCATTAGAGCTTCTGTTTCTGACAGATT 498
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Db 221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240
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Db 341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360
QY 1159 GAATCTATTGAAGAAGCTGACGGTTACTCTGCTTCTGGACTGTTCCATTCCGCTGCTAGA 1218
Db 361 GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380
QY 1219 GCTTACGTTGAATGCTCAATGCTCAAGCTGAAAGAACCATTCGTTAGAGTTTGGTT 1278
Db 381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400
QY 1279 AACGACAGAGTTGTTCCATTGACCGGTTGTGTTGTGACAGTTGGGTAGATGTAACAGA 1338
Db 401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420
QY 1339 GAGGACTTCGTTGAGGTTTGTCTTCGCTAGATCTGTTGGTAACTGGGAGAGATGTTTC 1398
Db 421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGluCysPhe 440
QY 1399 GPT 1401
Db 441 Ala 441

RESULT 4

US-09-121-425-2
: Sequence 2, Application US/09121425
: Patent No. 6153418
: GENERAL INFORMATION:
: APPLICANT: Lehmann, Martin
: TITLE OF INVENTION: Consensus Phytases
: FILE REFERENCE: Consensus phytases 13239
: CURRENT APPLICATION NUMBER: US/09/121.425
: EARLIER FILING DATE: 1998-07-23
: EARLIER APPLICATION NUMBER: EPO 97112688.3.

: EARLIER FILING DATE: 1997-07-24
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 467
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: consensus
: OTHER INFORMATION: sequence
: US-09-121-425-2

Alignment Scores:
Pred. No.: 2,696-204 Length: 467
Score: 2170.00 Matches: 416
Percent Similarity: 87.68% Conservative: 11
Best Local Similarity: 85.42% Mismatches: 20
Query Match: 87.29% Indels: 40
Gaps: 2

US-09-488-265B-30 (1-1404) x US-09-121-425-2 (1-467)

QY 1 ATGGGGGTGTTCTCGTGTACTGTCCATTGCCACCTTGTTGGTTCACATCCGTACC 60
Db 1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20
QY 61 GCCTTGGGTCCTCGTAACTCTCACTCTCTGTGCACACTGTTGACCGTGGTTACCAATCT 120
Db 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40
QY 121 TCCCCAGAAATTTCTCACTTGTGGGTATACATCTCCATCTCTCTCTCTCTCTCTCTCT 180
Db 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
QY 181 TCTGCTATTTCTCAGACGTTCCAAAGGGTGTAGAGTTACTTCTGCTCAAGTTTGTCT 240
Db 61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80
QY 241 AGACACGGTCTAGATACCCAACTTCTCTCGCTCTAAGCGGTACTCTGCTTGTATTGAA 300
Db 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla----- 97
QY 301 GCTATTCAAAGAAGCGTACTGCTTTCAAGGGTAACGCTTCTTGTGAAGACTTACAC 360
Db 98 -----ThrTyrAsn 100
QY 361 TACACTTGGGTGCTGACGACTTGACTCCATTCCGTTGCAACAACAAATGCTTAACTCTGT 420
Db 101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120
QY 421 ATTAAGTTCTACAGACATACAAGGCTTTGGCTAGAAAGATTGTCATTCATTATTAGACT 480
Db 121 IleLysPheTyrArgTyrTyrLysAlaLeuAlaArgLysIleValProPheIleAlaGla 140
QY 481 TCTGGTTCTCAGACAGTTATGCTTCTGCTGAAAGTTTCATTGAAGTTTCCAACTGCT 540
Db 141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160
QY 541 AAGTTGGTCAACCGAGTGTAAACCCACCAAGCTTCTCCAGTTATTATAC----- 591
Db 161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180
QY 592 -----GTTATTAT 600
Db 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200
QY 601 CCAGAAGGTCCTGTTTACAAACACACTTTGACACCGGTTGTTGCTACTGCTTTCGAAGA 660
Db 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY 661 TCTCAATTTGGGTGACGAGTTGAAGCTTAAGTTCACCTGCTTCTGCTCCACCAATTAGA 720
Db 221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Db 281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300
QY 901 AAGTACTAGCGGTACGGTCTGGTAACCCATTGGTCCAGCTCAAGGTGTGGTTCGTT 960
Db 301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValClyPheAla 320
QY 961 AACGAATTGATTGCTAGATTGACTCCTCCTCCAGTTCAGACCCACACTTCTACTAACCCAC 1020
Db 321 AsnGluLeuLeuAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCCATTTGCAATGGAAGCTGTAAGGCTGCTCTCT 1080
Db 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360
QY 1081 CACGACAACTATGTTTCTATTTCTTCGTTTGGTTTGTACAAAGGCTAAAGCCA 1140
Db 361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380
QY 1141 TTGCTACTACTCTGTTGTAATCTATTGAAGAACTGACGGTACTCTGCTCTTGGACT 1200
Db 381 LeuSerThrThrSerValGluSerIleGluThrAspGlyTyrSerAlaSerTrpThr 400
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QY 1261 TTGGTTAGAGTTTGGTTAAACAGACAGAGTGTTCATTGCCAGGTGTGGTGTGACAAAG 1320
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QY 1321 TTGGGTAGATGTAAAGAGACAGACTTCGTTGAAAGCTTTCCTTCGCTAGATCTGGTGT 1380
Db 441 LeuGlyArgCysLysArgAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGAAGATGTTTCGCT 1401
Db 461 AsnTrpAlaGluCysPheAla 467

RESULT 6

US-08-868-435-33
Sequence 33, Application US/08868435
Patent No. 6291221
GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868.435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/744,231
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc_feature
LOCATION: 104
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 119
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 205
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 228
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-868-435-33
Alignment Scores:
Pred. No.: 1,29e-176 Length: 465
Score: 2888.00 Matches: 359
Percent Similarity: 64.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
Gaps: 2
US-09-488-265B-30 (1-1404) x US-08-868-435-33 (1-465)
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Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 6: GCCTGGGTCCTCGTGAATCTCTACTCTGTGACACICTGTGACGGTGTACCAATGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TTCCAGAAATTTCTCAGTCTGCTGCTGCTACTCTCCATTCTCTCTTTGGCTGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTGTGAGACTTACTTTTCGTTCAAGTTTCTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGCACAGGTGCTAGATACCCAACTTCTCTCCGCTCTAAGCGGTACTCTGCTTTGATTGAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysLysLysLeuValThr 99
QY 301 GCTATTTCAAAGAACGCTACTGCTTTTCAAGGTAAGTACTGCTTTTGAAGACTTACAAC 360
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QY 361 TACACTTTGGGTGCTGACGACTTGCATTCCTCGGTGACCAACAATGTTTAACTCTGCT 420
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTCTTACACAGATACAAAGCTTTTGGCTAGAGAAGAITGTTCCATTCATTAGACT 480
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QY 541 AAGTTGCTCACCAGCTGCTAACCCACACCAAGCTTCCAGCTTATTAAAGCTTATTAT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAAGGTGCTGTTTCAACAACACTTTGGACACAGGGTTTGCTACTGTTTCCAGAA 650
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATGGGTGACGACGTTGAAGCTAACTTCACTGCTGCTTTTCCGCTCCACCAATTAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
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Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGACATATGTTCCATCGACACTGTTGGCTAGAACTTCTGACGCTACTCAATTTGCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCGTGCTACTGTTTCACTCAGCAGGATGATTCAATACGACTACTTGCATCTTTGGGT 900
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QY 901 AAGTACTACGGTTACGGTGTGTAAACCCATGGGTCACGCTCAAGGTGTGGTTTCGTT 960
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QY 961 AACGAATGATGCTAGATGACTCACTCTCCAGTTCAACACACGACTACTTACTACCCAC 1020
Db 319 AsnGluLeuIleAlaArgIleThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGACTCTTAACCCAGCTACTTCCCATTTGAAGCGTACTTTTGACGCTGACTTCTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CACGACAACTATGTTTCTTCTTCTTCCGCTTTGGGTTTGTACACGCTACTACGCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
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RESULT 7

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US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
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NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,231
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc_feature
LOCATION: 104
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
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LOCATION: 228
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 337
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-744-231-33
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Alignment Scores:
Pred. No.: 1,29e-176 Length: 465
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265B-30 (1-1404) x US-08-744-231-33 (1-465)

QY 1 ATGGCGGTGTTGCGTCTGCTACTGTCCATTGCCACCTTGTGCTGCCACATCCGGTACC 60

Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

QY 61 GCCTTGGTCCCTGGTAACCTCTGCTGACACTGTTGACGGTGTACCAAGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TTCACAGAAATTTTCACACTTGTGGGGTACACTCTCCATCTCTCTTTGGCTGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCAGAGCTTCCAAAGGCTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACAGGTGTAGATACCAACTCTCTTCGGCTTAAGGGGTAGTACGCTTCTTGAAGACTTACAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLeuLysLeuValThr 99
QY 301 GCTATTCAAAGCAAGCTACTGCTTTCAAAGGTAGTACGCTTCTTGAAGACTTACAA 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTGGTGGCTGACGACTTGACTCCATTCGCTGAACAACAATGTTAACTCTGCT 420
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
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Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIlele 198
QY 601 CCAGAGGTGCTGTTTACAAACACTTTGGACCAAGCTTTGGTACTGCTTTCGAGAA 660
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Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGGACATGTCCTCACTGACACACTTCTGACAGCTTCTGACGCTACTCAACTGCTTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCTGTGACTTCTCACTCACACGAATGGATTCAATACGACTACTTCAATCTTGTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 901 AGTACTAGGTTAGGCTGCTGTAACCCATTGGTCCAGCTCAAGGTGTGGTTTCGTT 960
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QY 961 AACGAATTCATTGCTAGATTGACTCACTCTCCAGTTCAAGCCACACTTCTACTACCA 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGAGCTCTAACCCAGCTACTTCCCAATTGAACGCTACTTTGTAGGCTGACTTCTC 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CAGGACAACACTATGGTTCATTCTTCGCTTTGGGTTTGTACACAGGCTACTAAGCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
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Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
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RESU:T 8
US-09-044-718-78
: Sequence 718, Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: CURRENT FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 78
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-09-044-718-78
Alignment Scores:
Pred. No.: 1,29e-176 Length: 465
Score: 1898.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 4 Gaps: 2
US-09-488-265B-30 (1-1404) x US-09-044-718-78 (1-465)
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Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLeuLysLeuValThr 99


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QY 541 AAGTTGGTGCACCGGTCCTAACCCACACACAGCTTCTCCAGTTATTAAAGCTTATTAT 600
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Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CAGGACAACTAAGTTCTATTCTTCGCTTTGGGTTTGTCAACGGTACTAAGCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY 1141 TTGTCTACTACTTCTCTCAATCTATTGAAGAACTGACGGTTACTCTGCTTCITGGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY 1201 GTTCCATTGCTGCTAGACCTTACGTTGAATGATGCAATGTGAAGCTGAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1261 TTGGTTAGAGTTTGGTTAACACAGAGTTGTTCCTCCACGGTTGGTGTTCACAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValProLeuHisGlyCysAspValAspLys 438
QY 1321 TTGGTTAGATGTAAGAGACGACCTCTGTTGAAGTTTGTCTTTTCGCTAGATCTGGTGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY 1381 AACTGGGAAGATGTTTCCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465
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RESULT 10
US-09-273-871A-8
; Sequence 8, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618,500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 8
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-273-871A-8

Alignment Scores:
Pred. No.: 1,29e-176 Length: 465
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
Gaps: 2
DB: 4

;;S-09-488-265B-30 (1-1404) x US-09-273-871A-8 (1-465)

QY 1 ATCGCGCGTGTTCGTCGTCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 61 GCCTTGGTCTCTCGTGTAACTCTCACCTCTGTGTGACACTGTTCAGGGTGGTACCAATGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TTCCCAAAATTCCTCACTTGTGGGTACATCTCTCCATCTCTCTCTCTTGGTGTGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCACAGCTTCCAAAGGTTGTAGAGTTACTTCTGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACACGGTGTAGATACCAACTCTTCGGTCTAAAGCGGTACTCTGCTTTGATTTAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLysLeuValThr 99
QY 301 GCTATTCAAAGAACGCTACTGCTTTCAGGGTAAGTACGCTTCTTGAAGACTTACAAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTrpAsn 119
QY 361 TACACTTTGGTGTGACGACTTGCATCCATTCGCTGAACCAACAAATGGTTAACTCTGT 420
Db 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAAGTTCTACAGCAATACAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGACT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGTTCTGACAGATTATTGCTTCTGCTGAAAGTTCAITGAAGGTTTCCCAATCTGT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
QY 541 AAGTTGGTGTACCAGGTGTAAACCCACACAGCTTCTCCAGTTATTAAAGTTATTATT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIlelle 198
QY 601 CCAGAAAGTCTGTTTACACACACACTTTCGACCCACCGTTCGTGTACTGCTTTCGAGAA 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTCGGTGACGACGTTGAAGCTAAGTCTCACTCTCTCTCTCTCTCTCTCTCTCT 720
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Db      219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY      721 GCTAGATTGGAGCTCACTGCCAGGTGTTAACTTGACTGACGAGAGGTGTTAACTTG 780
Db      239 AlaArgAlaGluLysHisLeuPheProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY      781 ATGGACATGTGCCATTCGACACACTGCTGCTAGAACCTTCGACGCTACTCAATGCTGCCA 840
Db      259 MetAspMetCysSerPheAspThrValAlaAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY      841 TTCTGTGACTTGTTCACCTACAGACCAATGGATTCACATACGACTACTTCCAATCTTTGGT 900
Db      279 PheCysGlnLeuPheThrHisAsnGlnTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY      901 AAGTACTACGGTTACGGTGGTGAACCCATGGGTCCAGCTCAGAGTGGTGGTTCGTT 960
Db      299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY      961 AACGAATTGATGCTAGATTGACTCACTCTCCAGTCAAGACCCACACTTCTACTAACCCAC 1020
Db      319 AsnGlnLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY      1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db      339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY      1081 CACGACACACATAGTTTCTATTTTCTTCGCTTGGGTTTGTACACGGTACTAAAGCCA 1140
Db      359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY      1141 TTGCTCTACTTCTGTTGAATCTATTGAAGAAACGACGGTTACTCTGCTTCTTGGACT 1200
Db      379 LeuSerArgThrSerValCysSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY      1201 GTTCATTCGCTGCTAGAGCTTACGTTGAATGTAGTGAATGTAGCTGAAGGAAAGAACCA 1260
Db      399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY      1261 TTGGTTAGAGTTTGGTTAAGCAGAGTGTGTCATTCGACGGTGTGGTGTGCTGACAA 1320
Db      419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY      1321 TTGGGTAGATGTAAAGACACGACTTCGTTGAAGTGTGCTTTCGCTAGATCTGCTGCT 1380
Db      439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY      1381 AACTGGGAAGATGTTGCT 1401
Db      459 AsnTrpGlyGluCysPheSer 465

RESULT 11
US-09-044-718-80
; Sequence 80, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSICHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WISS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
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US-09-044-718-80
Alignment Scores:
Pred. No.: 7,87e-176 Length: 465
Score: 1880.00 Matches: 358
Percent Similarity: 84.15% Conservative: 35
Best Local Similarity: 76.66% Mismatches: 72
Query Match: 75.62% Indels: 2
DB: Gaps: 4

US-09-488-265B-30 (1-1404) x US-09-044-718-80 (1-465)
QY      1 ATGGGCGTGTGCTGCTGCTACTGCTCAITGGCCACCTTGTTCGGTTCACCAICCGGTACC 60
Db      1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY      61 GCCTTGGTTCCTCGTGGTAACTCTCTGTCACACTCTTGACGACTCTTTCACGCGTGGTACC 120
Db      21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 35
QY      121 TTCGCAAAATTTCTCACTTGTGGGTACATCTCCCAITCTCTCTCTTCTTGGCTGACGAA 180
Db      40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY      181 TCTGCTATTTCTCCAGACGTTCCAAAGGTTGTAGAGTTACTTTCTGTTCAAGTTTGTCT 240
Db      60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY      241 AGACGCGTGTCTAGATACCCCACTTCTCTGCTCTAAGCGCTACTCTCTTGTGATTGAA 300
Db      80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99
QY      301 GCTATTCAAAGAACGCTACTGCTTTTCAAGGGTAAAGTACGCTTCTTGAAGACTTACAAC 360
Db      100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 419
QY      361 TACACTTTGGTGTGCTGACGACTTCACTCCATTCCGGTGAACAACAATGGTTAACTCTGGI 420
Db      120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 439
QY      421 ATTAAGTTCACAGACATACAAGGTTTGGCTGAGAAAGATTGCTTCATTCATTCATGAGCT 480
Db      140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 459
QY      481 TCTGTTCTCACAGAGTATTGCTTCTGCTGAAAAAGTTCATTCAAGGTTTCCCAATCTGCT 540
Db      160 SerGlySerAspArgValIleAlaSerGlyGluTyrPheIleGlyPheGlnGlnAla 479
QY      541 AAGTTGCTGACCCAGGTGCTTAACCCACACCAAGCTTCTCCAGTTATTACGTTATTATT 600
Db      180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 496
QY      601 CCAGAAGGTCGTGTACACACACACTTTTCGACACCGTTTGTGTACTGCTTTCGAGAA 660
Db      199 ProGlnSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY      661 TCTGAATTGGGTGACGAGCTTGAAGCTTAACCTTCACCTGCTGTTTTCGCTCCACCAATAGA 720
Db      219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY      721 GCTAGATTGGAAGCTCACTTCCAGGTGTTAACTTGACTGACGAGAGGTGTTAACTTG 780
Db      239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY      781 ATGCACATGTCTCCATTCGACACTGTTGTGCTAGAACTTCTGACGCTACTCAATGCTCCCA 840
Db      259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY      841 TTCTGTGACTTGTTCACCTACGACGAGTGAATTCACATACGACTACTTCCAATCTTTGGT 900
Db      279 PheCysGlnLeuPheThrHisAsnGlnTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY      901 AAGTACTACGGTTACGGTGGTGAACCCATGGGTCCAGCTCAGAGTGGTGGTTCGTT 960
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Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATGATGCTAGATCACTCACTCCAGGTTCAAGACACACACTTCTACTAACCCAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCT 1060
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAlaPheSer 358
QY 1081 CAGCACAACTATGTTTCTATTTTCTCGCTTTGGGTTGTACACGGTACTACACCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY 1141 TTGTCTACTTCTCTGTTGAATCTATTGAACAACTACCGGTACTCTCTCTCTGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaGlyGluLeuAspGlyTyrSerAlaSerIrrVal 398
QY 1201 GTTCCATTGCTGTAGAGCTTACGTTGTTCAATGATCAATGTGAAGCTGAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluSer 418
QY 1261 TTGTTAGAGTTTGGTTACGCACAGAGTTGTTCCATTGACGGTTCTGGTGTGTGACAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1321 TTGGGTAGATTAAGACAGAGCACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY 1381 AACTGGGAAGAAATGTTTCGCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465
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RESULT 12

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US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCH, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-79
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Alignment Scores:
Pred. No.: 9,86e-176 Length: 465
Score: 1879.00 Matches: 358
Percent Similarity: 84.15% Conservative: 35
Best Local Similarity: 76.66% Mismatches: 72
Query Match: 75.58% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265B-30 (1-1404) x US-09-044-718-79 (1-465)

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Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
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Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TCTGTATTTCCTCCAGACGCTTCCAAAGGCTTTAGAGTTACTTTCGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACCGGTGCTAGATACCACTTCTCTCGCTCTAAGCGCTACTCTCTCTGTTGTA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysLysLysLysLysValThr 99
QY 301 GCTATTCAAAAAGAACGCTACTGCTTTCAGAGGTAGTAGCTTCTTGAAGACTTACAAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTGGGTGCTCAGCACTTGACTCCATTCGGTGGTGAACACAAATGTTAACTCTGT 420
Db 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTTCTACAGAAGATACAGGCTTTGGCTAGAAAGATTGTTCCATTCTTAGAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGGTTCTGACAGAGTTATTGCTCTGCTGATAAAGTTCAATTGAAGGTTTCCAATCTGT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGlyLysPheIleGluGlyPheGlnAla 179
QY 541 AGTTTGGCTGACCCAGGTGCTTAACCCACACCAAGCTTCTCCAGTTATTAACTGTTATT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAAAGTGTGCTGTACAAACACTTTGGACCAAGGTTTGTGTACTGCTTTCGAAGAA 560
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTTGGTGACGACGCTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAACCTCAGTTGCCAGGTGTAACTGACTGACGACGACGCTTGTAACTTG 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGGACATGTGCTCATTCGACACTGTTGTAGAACTTCTGACGCTACTCAATGTCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCTGTGACTTGTTCCTACTCAGCAGCAATGGATTCAATAGACTACTTGAATCTTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGGTTACGTCGTCGTAACCATTCGGTCCAGCTCAAGCTCTGTTTCGTT 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATGATGCTAGATTGACTCACTCTCCAGTTCAAGACACACACTTCTACTAACCCAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CAGCACAACTATGTTTCTATTTTCTTTCGCTTTCGGTTCGTTCACACGGTACTACGCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluGly 378
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Db 249 ArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValSerLeuMet 268
Qy 784 GACATGTGTCATTGCACACTGTCGCTAGAACTTCTGCAGCTACTGAATTGCTCCATTC 843
Db 269 AspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerProPhe 288
Qy 844 TGCTGTTTGTCTACTCAGCAGCAATGGATCCAACTACGACTACTTGCAGAGCTTGGGTAAG 903
Db 289 CysGlnLeuPheThrHisAsnGluTrpLysLysThrAsnTyrLeuGlnSerLeuGlyLys 308
Qy 904 TACTACGGTTACGGTCTGCTGAACCAATGGGTCCAGCTCAAGGTGTGGTTTCGCTAAC 963
Db 309 TyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyLeuGlyPheThrAsn 328
Qy 964 GAATGTATGCTAGATGACTCACTCTCCACTCTCAAGCACCACACTTCTACTAACCACACT 1023
Db 329 GluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSerThr 346
Qy 1024 TTGGACTCTAACCCAGCTACTTCCCAITGAACGCTACTTGTACGCTGACTTCTCTCAC 1083
Db 349 LeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSerHis 368
Qy 1084 CACACACTATGATCTATTCTTCGCTTTGGGTTGTACACGCTACCAAGCCATTG 1143
Db 369 AsnAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeu 388
Qy 1144 TCTACTACTCTGTGTGAATCTATTGAAGAACTGACGGTTACTCTGCTTCTTGACACTG 1203
Db 389 SerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValVal 408
Qy 1204 CCATTCGCTGTAGAGCTTACGTTGAAGAIGATGCAATGTCAGTCAAGTGAAAGAACCATTC 1263
Db 409 ProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluProLeu 428
Qy 1264 GTTAGAGTTTGGTTAAGCAGACTTCTTCCATTGCGCTGCTGCTGTGTGACAAGTTG 1323
Db 429 ValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLysLeu 448
Qy 1324 GGTAGATGAAGAGAGAGCACTTCGTTCAAGGTTGTCTTTTCGCTAGATCTGGTGGTAAC 1383
Db 449 GlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsn 468
Qy 1384 TGGCGTGAATGTTTCGCT 1401
Db 469 TrpGlyGluCysPheSer 474

RESULT 9

Sequence 3, Application US/09929060
Patent No. US20020068350A1
GENERAL INFORMATION:
APPLICANT: KONDO, HIDEMASA
APPLICANT: ANAZAWA, HIDEHARU
APPLICANT: KANEKO, SYUNICHI
APPLICANT: NAGASHIMA, TADASHI
APPLICANT: TANGE, TAISUFA
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 081356/0166
CURRENT APPLICATION NUMBER: US/09/929,060
CURRENT FILING DATE: 2001-08-05
PRIORITY APPLICATION NUMBER: 09/543,744
PRIORITY FILING DATE: 2000-04-05
PRIORITY APPLICATION NUMBER: 09/155,855
PRIORITY FILING DATE: 1998-10-05
PRIORITY APPLICATION NUMBER: JP 084314/1996
PRIORITY FILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 467
TYPE: PRT
ORGANISM: Aspergillus niger
us-09-929-060-3

Alignment Scores: 3.59e-151 Length: 467
Pred. No.: 1850.00 Matches: 346
Score: 84.37% Conservative: 48
Best Local Similarity: 74.09% Mismatches: 73
Query Match: 75.00% Indels: 0
DB: 9 Gaps: 0
US-09-488-265B-28 (1-1404) x US-09-929-060-3 (1-467)
Qy 1 ATGGGGGIGTTCGTGCGTACTGTCCATGTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuSerGlyValThrSerGlyLeu 20
Qy 61 GCCTTGGGTCCTCGTGAATTCCTACTCTTGTGACACTGTTGACGGTGTTCACCAAGT 120
Db 21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyTyrGlnCys 40
Qy 121 TTCCAGAAATTTCTCAGCTTGTGGGTACCTACTCTCCATCTCTCTTGGCAGACGAA 180
Db 41 PheSerGluThrSerHisLeuIrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnLys 60
Qy 181 TCTGCTATTCTCCAGAGCTTCCAGAGCTGTAGAGCTTACTTTCGTTCAAGTTTGTCT 240
Db 61 SerAlaIleSerProAspValProAlaGlyCysHisValThrPheAlaGlnValLeuSer 80
Qy 241 AGACAGGTCGTAGATACCAACTTCTTCTCGCTCTAAGGCTTACTCTGCTTGTGATTGA 300
Db 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
Qy 301 GCTATTCAAAGAACGCTACTGCTTCAAGGTAAGTACGCTTCTTGTGAAGACTTACAA 360
Db 101 GluIleGlnGlnAsnAlaThrThrPheGluGlyLysTyrAlaPheLeuLysThrTyrAsn 120
Qy 361 TACACTTTGGGTGCTGAGACTTGCCTCCATTCGTTGGTGAAGAACCAATGTTTACTCTG 420
Db 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
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Qy 481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAGTTTCAATGAAGGTTTCCAACTGCT 540
Db 161 SerGlySerSerArgValIleAlaSerGlyAsnLysPheIleGluGlyPheGlnSerThr 180
Qy 541 AAGTTGCTGACCCAGGTTCTCAACACACACCAAGTCTCCAGTTATTACGTTGATCAT 600
Db 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValle 200
Qy 601 CCAGAAGGATCCGGTTTACAACAACACTTTGGACCCAGGTACTTGTACTGCTTTCGAAGAC 660
Db 201 SerGluAlaSerThrSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
Qy 661 TCTGAATTAGGTGACGAGCTTGAAGCTTAATTCACGTCGTTTTCGCTCCAGCTATTAGA 720
Db 221 SerGluLeuAlaAspAspIleGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
Qy 721 GCTAGATTGAAGCTGACTTGCAGGTTGCTTACTTGTACTGACACCAAGACGTTGTTACT 780
Db 241 GlnArgLeuGluAsnAspLeuSerGlyValSerLeuThrAspThrGluValThrTyrLeu 260
Qy 781 ATGGACATGTGTCATTCGACACTGTGCGTGAAGACTTCTGACGCTACTGAATTTGCTCCA 840
Db 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
Qy 841 TTCTGTGCTTTGTTTCACTACGACGAGTATGGATCCAAATACGACTACTTGCAGACCTGG 900
Db 281 PheCysAspLeuPheThrHisGluGluTrpIleAsnTyrAspTyrLeuGlnSerLeuAsn 300
Qy 901 AAGTACTACGGTTACGGTGTGTGTAACCCATTGGTCCACGCTCAAGCTGTGTTGCTTCG 960
|||||


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QY 1141 TTGCTACTACTTCTGTTGAATCTATTGAAGAAGCTGACGGTTACTCTCTCTTCTGGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY 1201 GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluSer 418
QY 1261 TTGGTTAGAGTTTGGTTAACGACAGAGTGTGTTCCATTGACCGGTTGTGCTGTTGACAAG 1320
Db 419 LeuValArgAlaLeuLeuAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1321 TTGGGTAGATGTAGACAGACGACTTCGTTGAAGGTTTCTTCCGCTAGATCTGGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY 1381 AACTGGGCTGAATGTTTCGGT 1401
Db 459 AsnTrpGlyGluCysPheSer 465

RESULT 11
US-10-062-848-79
: Sequence 79, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062.848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 79
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-10-062-848-79

Alignment Scores:
Pred. No.: 5,33e-151 Length: 465
Score: 1858.00 Matches: 354
Percent Similarity: 83.51% Conservative: 36
Best Local Similarity: 75.80% Mismatches: 75
Query Match: 74.92% Indels: 2
DB: 15 Gaps: 2

US-09-488-265B-28 (1-1404) x US-10-062-848-79 (1-465)
QY 1 ATGGGGGTGTTGCTGCTACTGCTACTGCTATTCACCTGTTGCTGCTCCACATCCGGTACC 60
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 61 GCCTTGGGCTCGTGGTAAATCTCACTCTGTGACACTGTTGACGGTGTACCAATGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TTCACGAAATTTCTCACTTGTGGGGTACCTTCTCTCCATCTCTCTTTTGGCAGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCAGAGCTTCCACAGACGTGTAGAGTTACTTTCTGGTTCAGTTGTGCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
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QY 241 AGACACGGTGTAGATACCAACTTCTTCGGTCTTAAGGCTTACTCTCTCTTIGATTGAA 300
Db 80 ArgHisGlyAlaArgIyrProThrSerLysSerLysLysLysLysLysLysLysLysLys 99
QY 301 GCTATTCAAAAGAACCTACTGCTTTCAAGGGTAGTAGCTGCTTTCTTGAAGACTTTACAAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAGGTAACCAATGTTTAACTCTGCT 420
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTTCTACAGAGATACAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTTCATTGAAGGTTTCCAATCTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179
QY 541 AGTTGGTGTACCCAGGTTCTCAACACACACAGGCTTCTCCAGTTATTAACTGATCAT 600
Db 180 LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAAAGGATCCGGTTACAAACACACTTTGGACCCAGGTTACTTGTACTGCTTTCGAAGAC 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACGTCTTGTTCGCTCCAGCATTAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAAGCTGACTTGGCAGGTGTACTTTGACTGACGAAACGCTTCTTTACTTG 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGCACATGTGTCATTCGACACTGCTCGGTAGAACTTCTGAGGCTACTGAANTTGCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TCTGCTGCTTTGTTCACTCACGACGAATGGATCCAACTACGACTACTTGCAGGCTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGGTTACGGTACCCATTCGGTCCAGCTACGCTCAAGCTGTGTGTTTCGCT 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATTGATTGCTAGATTGACTCTCTCCAGTTCAAGACACACACTTCTTACTAACCA 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCCATTTGACGCTACTTTGACGCTGACTTCTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CACGACAACTATGATATCTATTTCTTCGCTTTGGTTTGTACAAAGCTTACCAAGCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluGly 378
QY 1141 TTGCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTCTCTTCTGGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY 1201 GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1261 TTGGTTAGAGTTTGGTTAACGACAGAGTGTGTTCCATTGCTGCTGTTGACAAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
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;; CURRENT APPLICATION NUMBER: US/10/062,848

;; PRIOR FILING DATE: 2002-02-01

;; PRIOR APPLICATION NUMBER: 09/044,718

;; PRIOR FILING DATE: 1998-03-19

;; PRIOR APPLICATION NUMBER: EP 97810175.6

;; PRIOR FILING DATE: 1997-03-25

;; NUMBER OF SEQ ID NOS: 82

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 12

;; LENGTH: 449

;; TYPE: PRT

;; ORGANISM: Aspergillus fumigatus

US-10-062-848-12

Alignment Scores:

Pred. No.: 5,79e-151 Length: 449

Score: 1857.50 Matches: 347

Percent Similarity: 87.05% Conservative: 36

Best Local Similarity: 78.86% Mismatches: 56

Query Match: 74.90% Indels: 1

DB: 15 Gaps: 1

US-09-488-265b-28 (1-1404) x US-10-062-848-12 (1-449)

QY 82 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCAGAAATTTCTCACTTG 141

DB 11 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 30

QY 142 TGGGTACTACTCTCCATCTCTCTTTGGCAGCAGCAATCTGTAATTTCTCCAGAGTT 201

DB 31 TrpGlyGlnTyrSerProPheSerLeuGluAspGluLeuSerValSerSerLysLeu 50

QY 202 CCAGCAGACTCTAGACTTACTTCTGTTCAAGTCTTGTCTAGCACGGTGTAGATACCCA 261

DB 51 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgIlePro 70

QY 262 ACTTCTTCTCGTCTAAGGCTTACTCTCTGTTGATTGAAGCTATTCAAAAGAACGCTACT 321

DB 71 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 90

QY 322 GCTTTCAGGGTAAGTACGCTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 381

DB 91 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 110

QY 382 TTGACTCCACTCGGTGAAACAAATGTTAACTCTGTTAACTTAACTTCTCAGAGATAC 441

DB 111 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 130

QY 442 AAGCTTTGGCTAGAAAGATTGTTCCATTCAATAGAGCTTCTGGTTCGACAGAGTTATT 501

DB 131 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 150

QY 502 GCTTCTGCTGAAAGTTTCAATGAGGTTTCAATGCTAGTGGTGGTGGTGGTGGTGGTGGT 561

DB 151 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 170

QY 562 CAACACACCAAGCTTCTCAGTATTACCTGATCATTCACGAAGGATCCGGTTACAAAC 621

DB 171 ---ThrAsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 189

QY 622 AACACTTTGGACCGGCTACTGTACTCTTCCAGACTCTGAATTAGGTGACGAGCTT 681

DB 190 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 209

QY 682 GAAGCTACTTCACTGCTTGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTG 741

DB 210 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaAlaGluLysHisLeu 229

QY 742 CCAGGTGTTACTTTGACTGACGAGACCTGTTTACTTGTGATGGACATGTGCTCATTCGAC 801

DB 230 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 249

QY 802 ACTGTGCTAGAACTTCTGAGGCTACTGAATTTGTTCTCCATTTCTGCTTTGTTCACTCAC 861

DB 250 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 269

QY 862 GACGAATGATCCAAATAGCACTACTTGCAGGCTGGTAAGTACTACGGTTACGGTGCT 921

DB 270 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 289

QY 922 GGTAAACCATTTGGTCCAGCTCAAGGTGTTGGTTTCGCTAACCAATTTGATTGCTAGATTG 981

DB 290 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 309

QY 982 ACTCACTCTCCAGTTCAGACACCACTTCTACTAACCACTTTGGACTTTAAACCCAGCT 1041

DB 310 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 329

QY 1042 ACTTTCATTCGACGCTACTTGTAGCGCTGACITCTCTCCACGACACACTATGATATCT 1101

DB 330 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnMetValSer 349

QY 1102 ATTTTCTCGCTTTGGTGTACAAAGCGGTACCAAGCCATGTCTACTACTTCTGTTGAA 1161

DB 350 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgIleSerValGlu 369

QY 1162 TCTATTGAAGAACTGACGCTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCT 1221

DB 370 SerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValValProPheGlyAlaArgAla 389

QY 1222 TACGTTCAAATGATCCAACTGCAAGCTGAAAGAACCACTTGTGTACAGTTTGGTTAAC 1281

DB 390 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 409

QY 1282 GACAGAGTTGTCCTTCCATTCGACGCTGTGCTGTTGACAAGTTGGTGTAGATGTAAGAGAGAC 1341

DB 410 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 429

QY 1342 GACTTCGTTCAAGGTTTGTCTTTCGCTAGATCTGTTGTTAACTGGGCTGAATGTTGCT 1401

DB 430 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 449

RESULT 14

US-10-062-848-81

;; Sequence 81, Application US/10062848

;; Publication No. US20030092155A1

;; GENERAL INFORMATION:

;; APPLICANT: KOSTREWA, Dirk

;; APPLICANT: PASAMONTES, Luis

;; APPLICANT: TOMSCHY, Andrea

;; APPLICANT: van LOON, Adolphus

;; APPLICANT: VOGEL, Kurt

;; APPLICANT: WYSS, Markus

;; TITLE OF INVENTION: MODIFIED PHYTASES

;; FILE REFERENCE: Modified Phytases

;; CURRENT APPLICATION NUMBER: US/10/062,848

;; CURRENT FILING DATE: 2002-02-01

;; PRIOR APPLICATION NUMBER: 09/044,718

;; PRIOR FILING DATE: 1998-03-19

;; PRIOR APPLICATION NUMBER: EP 97810175.6

;; PRIOR FILING DATE: 1997-03-25

;; NUMBER OF SEQ ID NOS: 82

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 81

;; LENGTH: 465

;; TYPE: PRT

;; ORGANISM: Aspergillus fumigatus

US-10-062-848-81

Alignment Scores:

Pred. No.: 9.64e-151 Length: 465

Score: 1855.00 Matches: 353

Percent Similarity: 83.51% Conservative: 37

Best Local Similarity: 75.59% Mismatches: 75

Query Match: 74.80% Indels: 2

DB: 15 Gaps: 2

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US-09-488-265B-28 (1-1404) x US-10-062-848-81 (1-465)
QY 1 ATGGGCGTTCGTCGTCTACTGTCCATTCGCACCTTGTTCGGTCCACATCCGGTACC 60
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 61 GCCTTGGGTCCTCGTGAATTCCTACTCTCTGTGACACTGTTGACGGTGGTACCAATGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TTCCAGAAATTTCTCAGTGTGGGTACTACTCTCCATACTCTCTTTGGCAGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACCGGTGCTAGATACCAACTTCTTCTGCTCTAAGGCTTACTCTCTGTTGATTGAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValInr 99
QY 301 GCTATTCAAAAGAACGCTACTGCTTCAAGGTAAGTACGCTTCTTGAAGACTTCAAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGTTGGTAAACCAATGCTTAACCTGCT 420
Db 120 TyrThrLeuGlyAlaAspAspLeuThrAlaPheGlyGluGlnCnleuValAsnSerGly 139
QY 421 ATTAAGTCTTACAGAGATACAAAGGCTTTGGCTAGAAAGATTGTTCCATTTCATAGAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGGTCTCAGACAGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
QY 541 AAGTTGGCTCACCAGGCTTCTCAACACACCAAGCTTCTCCAGTTTAACTGATGATCAT 600
Db 180 LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleLe 198
QY 601 CCAGAGGATCCGGTTACAAACACACTTTGGACCCAGGTAAGTGTACTGCTTTCGAAGAC 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCCACTGCTTGTGCTCCAGCTATTAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAAGCTGACTTGGCAGGTGTTACTTTGACTGACGAGACGTTGTTTACTTG 780
Db 239 AlaArgAlaLysLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGACATGTCTCCATTCGACACTGTCGCTAGACTTCTGACGCTACTGAAATGCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCTGTGCTTTGTTCACTACGACGAAATGATCCAATACGACTACTTGAAAGCTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGGTTACGGTGTGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATTGATTGCTAGATTGACTACTCTCCAGTTCAGACACGACTTCTTACTACCCAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGGACTCTACCCAGCTACTTTCCCAATTCAGCGCTACTTTGTACGCTGACTTCTCT 1080
Db 1080
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339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
1081 CACGACACACTATCATATCTATTTCTTCGCTTTGGCTTTCTACACGGGTACCAAGCCA 1140
Db 359 HisAspAsnSerMetValSerIlePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
1141 TTGCTACTACTTCTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
1201 GTTCATTTCGCTGCTAGAGCTTACGTTGAATGATGCAATGTCAAGCTGAAAGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
1261 TTGGTTAGAGTTTGGTTAAGCAGACAGTGTTCATTGACGAGTGTGCTGTTGACAAAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
1321 TTGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGCTGCT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
1381 AACTGGGCTGAATGTTTCGCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465
RESULT 15
US-10-229-358-12
; Sequence 12, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC386-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version. 4.0
; SEQ ID NO 12
; LENGTH: 462
; TYPE: PKT
; ORGANISM: Aspergillus niger
US-10-229-358-12
Alignment Scores:
Pred. No.: 2,12e-150 Length: 462
Score: 1851.00 Matches: 349
Percent Similarity: 84.42% Conservative: 41
Best Local Similarity: 75.54% Mismatches: 72
Query Match: 74.64% Indels: 0
DB: 15 Gaps: 0
US-09-488-265B-28 (1-1404) x US-10-229-358-12 (1-462)
QY 1 ATGGGCGTTCGTCGTCTACTGTCCATTCGCACCTTGTTCGGTCCACATCCGGTACC 60
Db 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20
QY 61 GCCTTGGTTCCTCGTGGTAATTCCTACTCTCTGTGACACTGTTGACGGTGGTACCAATGT 120
Db 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TTCCAGAAATTTCTCAGTGTGGGTACTACTCTCCATACTCTCTTTGGCAGACGAA 180
Db 41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
QY 181 TCTGCTATTCTCCAGACGTTCCAGACGACTTCCAGCTACTTCTGCTTCAAGTTTGTCT 240
Db 181
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Db 61 ServallieserProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY 241 AGACACGGTGTAGATACCCAACTTCTTCTCGGTCTAAGGCTTACTCTGCTTTAATTGAA 300
Db 8 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGACGCTACTGCTTCTCAAGGTAAGTACGCTTCTTCAAGACATACAAAC 360
Db 101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTTGGGTGCTGACAGCTTGCATTCATTCGGTGAAGAACCAATGGTTAACTCTGGI 420
Db 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAAGTCTTACAGAGATACAAAGCTTTGGCTAGAAAGATGTTCCATTCATTTAGAGCT 480
Db 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 560
QY 481 TCTGGTCTGACAGAGTTATTGCTTCTGCTGAAGATTCATTGAAGGTTTCCAACTCTGCT 540
Db 161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180
QY 541 AAGTTGGCTGACCCAGGTTCTCAACACACACCAAGCTTCTCCAGTATTAACTGATCATC 600
Db 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200
QY 601 CCAGAAGGATCCGGTTACAAACACACTTTGGACACGGTACTTGTACTGCTTTCGAAGAC 660
Db 201 SerGluAlaSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATTAGGTGACGACCTGAAGCTAACTTCACTGCTTGTCTGCTCCAGCTATFAGA 720
Db 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheAlaProSerIleArg 240
QY 721 GCTAGATTGGAAGCTGACTTCCAGCTGTTACTTTGACTGACGAAGACGCTTCTTACTTG 780
Db 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
QY 781 ATGGACATGTCCTCATTCGACACACTGCTGCTAGAACTTCIGACGCTACTGAATTGCTCCA 840
Db 261 MetAspMetCysSerPheAspThrIleSerThrIleSerThrValAspThrLysLeuSerPro 280
QY 841 TCTGTGCTTCTTCACTCAGCAGCAATGGATCCCAATACGACTACTTGCAAAAGCTTGGGT 900
Db 281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
QY 901 AAGTACTAGGTTACGGTCTGGTAACCCATGGGTCCAGCTCAGGCTGTTGGTTCTGCT 960
Db 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY 961 AACGAATTGATTGCTAGATTGACTACACTCTCCAGTTCAGACACACTTCTACTAACCCAC 1020
Db 321 AsnGluIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340
QY 1021 ACTTTGGACTCTAACCCAGCTACTTTCCGATTGACGCTACTTTGACGCTGACTTCTCT 1080
Db 341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
QY 1081 CAGCACAACACTATGATATCTATTTCTTCGCTTTGGGTTTGTACACCGGTACCAAGCCA 1140
Db 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
QY 1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTCTTCTTGGACT 1200
Db 381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaIleThr 400
QY 1201 GTTCCATTCGCTGCTAGAGCTTACGTGAAATGATGCAATGCAAGCTGAAAGGAACCA 1260
Db 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420
QY 1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTCGACGGTTGCTGCTGTGACAAS 1320
Db 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

QY 1321 TTGGTACATGTAAAGACAGACGACITCGTTGAAGGTTTGTCTTCCTAGATCTGGTGGT 1380
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QY 1381 AACTGG 1386
Db 461 AspTrp 462

Search completed: October 3, 2003, 09:05:52
Job time : 94.6311 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 07:48:21 ; Search time 21.0567 Seconds
(without alignments)
5642.336 Million cell updates/sec

Title: US-09-488-265B-28
Perfect score: 2480
Sequence: 1 atgggcgtgttcgtcgtact.....gggctgaatgttcgcttaa 1404

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 326717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=oct3.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=huma:4C.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2408	97.1	467	4	US-09-273-871A-9 Sequence 9, Appli
2	2282	92.0	441	3	US-09-121-425-1 Sequence 1, Appli
3	2282	92.0	441	4	US-09-634-493A-1 Sequence 1, Appli
4	2270	91.5	467	3	US-09-121-425-2 Sequence 2, Appli
5	2270	91.5	467	4	US-09-634-493A-2 Sequence 2, Appli
6	1879	75.8	467	1	US-07-923-724-8 Sequence 8, Appli
7	1879	75.8	467	2	US-08-609-426A-8 Sequence 8, Appli
8	1879	75.8	467	1	US-08-374-652C-2 Sequence 2, Appli
9	1875	75.6	467	1	US-08-151-574-32 Sequence 32, Appli
10	1875	75.6	467	1	US-08-146-424-20 Sequence 20, Appli
11	1875	75.6	467	1	US-08-693-709-2 Sequence 2, Appli
12	1875	75.6	467	2	US-08-419-448-32 Sequence 32, Appli

13	1875	75.6	467	2	US-08-819-825-3 Sequence 3, Appli
14	1875	75.6	467	3	US-09-163-842-3 Sequence 3, Appli
15	1875	75.6	467	4	US-09-233-510-32 Sequence 32, Appli
16	1875	75.6	467	4	US-09-636-499-5 Sequence 5, Appli
17	1867	75.3	465	3	US-08-868-435-33 Sequence 33, Appli
18	1867	75.3	465	4	US-08-744-231-33 Sequence 33, Appli
19	1867	75.3	465	4	US-09-044-718-78 Sequence 78, Appli
20	1867	75.3	465	4	US-09-636-499-6 Sequence 6, Appli
21	1867	75.3	465	4	US-09-273-871A-8 Sequence 8, Appli
22	1863	75.1	467	4	US-09-273-871A-11 Sequence 11, Appli
23	1860	75.0	467	3	US-09-155-855-3 Sequence 3, Appli
24	1860	75.0	467	4	US-09-543-744-3 Sequence 3, Appli
25	1860	75.0	467	4	US-09-929-060-3 Sequence 3, Appli
26	1859	75.0	465	4	US-09-044-718-80 Sequence 80, Appli
27	1858	74.9	465	4	US-09-044-718-79 Sequence 79, Appli
28	1857.5	74.9	439	4	US-09-044-718-3 Sequence 3, Appli
29	1857.5	74.9	449	4	US-09-044-718-12 Sequence 12, Appli
30	1855	74.8	465	4	US-09-044-718-81 Sequence 81, Appli
31	1851	74.6	462	4	US-09-636-499-12 Sequence 12, Appli
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33	1839	74.2	466	3	US-08-866-435-35 Sequence 35, Appli
34	1839	74.2	466	4	US-08-744-231-35 Sequence 35, Appli
35	1835.5	74.0	463	3	US-08-868-435-29 Sequence 29, Appli
36	1835.5	74.0	463	4	US-08-744-231-29 Sequence 29, Appli
37	1835.5	74.0	463	4	US-09-273-871A-10 Sequence 10, Appli
38	1833	73.9	444	4	US-09-044-718-1 Sequence 1, Appli
39	1820.5	73.4	447	4	US-09-044-718-6 Sequence 6, Appli
40	1818	73.3	443	3	US-09-155-855-1 Sequence 1, Appli
41	1818	73.3	443	4	US-09-543-744-1 Sequence 1, Appli
42	1818	73.3	443	4	US-09-929-060-1 Sequence 1, Appli
43	1813	73.1	443	3	US-09-155-855-2 Sequence 2, Appli
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ALIGNMENTS

RESULT 1
US-09-273-871A-9

; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618 500-US
; CURRENT APPLICATION NUMBER: US/09/273.871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080.129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090.675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Alignment Scores:
Pred. No.: 2.7e-236 Length: 467
Score: 2408.00 Matches: 457
Percent Similarity: 98.50% Conservative: 3

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Best Local Similarity: 97.86% Mismatches: 7
Query Match: 97.10% Indels: 0
DB: 4 Gaps: 0

US-09-488-265B-28 (1-1404) x US-09-273-871A-9 (1-467)

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DB 61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 60
QY 241 AGACACGGTGTACATACCAACTCTCTCCGCTCAAGCTTACTCTGCTTTGATGAA 300
DB 81 ArgHisGlyAlaArgTyrserProtyrPheSerLysAlaTyrserAlaLeuLeuGlu 300
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DB 101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrsAlaPheLeuLysThrTyrsn 120
QY 361 TACACTTTGGGTGCTGAGCTTCACTCCATTCGGTGAAGAACCAATGGTTACTCTGGT 420
DB 121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140
QY 421 ATTAAGTCTACACAAATACAAAGCTTGGCTAGAAGATTTGCCATTCATTAGAGCT 480
DB 141 IleLysPheIleArgArgTyrsAlaLeuAlaArgLysIleValProPheIleArgAla 160
QY 481 TCTGGTCTCAGAGATTATGCTCTGCTGAAAGTTTCATGAAGTTTCCAACTCTGCT 540
DB 161 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180
QY 541 AAGTGGCTGACCCAGGTCTCAACACACCAAGCTTCTCCAGTTATACGGTATCATT 600
DB 181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIle 200
QY 601 CCAGAAGATCCGGTTACAAACACACTTGGACACCGTACTTGTACTGCTTTCGAAGAC 660
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QY 661 TCTGAATAGGTGACGAGTGAAGCTAACTTCACTGCTTGTTCGCTCCAGCTATTAGA 720
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QY 721 GCTAGATTGGAAGCTGACTTCCAGGTGTACTTGTACTGACGAAGAGTGTTCATTCTG 780
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QY 781 ATGGACATGTGTCCATTCGACACTGTCGGTAGAAGCTTCTGACGCTACTGAATGTCTCCA 840
DB 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
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RESULT 2
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; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus Phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; EARLIER FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-1

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QY 319 ACTGCTTCCAAAGGTAAGTACGCTTCTTGAAGACTTACAACTACACACTTGGTGTGAC 378
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QY 379 GACTTGACTCCATTCGGTGAACCAAAATGGTTAACTCTGGTATTAAAGTTCTACAGAGA 438
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Db 361 GluSerIleGluThrAspGlyTyrSerAlaSerTyrThrValProPheGlyAlaArg 380
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QY 1279 AACGACAGAGTTCTTCCATTGACCGTTGCTGTTGACAAAGTTGGGTACATGTAAAGAGA 1338
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Db 441 Ala 441
RESULT 3
US-09-634-493A-1
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: Patent No. 6579975
: GENERAL INFORMATION:
: APPLICANT: Lehmann, Martin
: TITLE OF INVENTION: Consensus Phytases
: FILE REFERENCE: consensus phytases 13239
: CURRENT APPLICATION NUMBER: US/09/634.493A
: CURRENT FILING DATE: 2000-08-08
: PRIOR APPLICATION NUMBER: US/09/121.425
: PRIOR FILING DATE: 1998-07-23
: PRIOR APPLICATION NUMBER: EPO 97112688.3
: PRIOR FILING DATE: 1997-07-24
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 441
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: consensus
: OTHER INFORMATION: sequence
US-09-634-493A-1
Alignment Scores:
Pred. No.: 1,75e-223 Length: 441
Score: 2282.00 Matches: 431
Percent Similarity: 98.41% Conservative: 3
Best Local Similarity: 97.73% Mismatches: 7
Query Match: 92.02% Indels: 0
DB: 4 Gaps: 0
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Db 1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGluIleSerHis 20
QY 139 TTGTGGGTGACTTACTCTCCATCTTCTTCTTGGCAGACGAACTCTGCTATTCTCCAGAC 198
Db 21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40
QY 199 GTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTGTCTAGACACGGTGTGCTAGATAC 258
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QY 259 CCAACTTCTTCTGCTCTAAGCCTTACTCTGCTTGTGTTGAGCTATTCAAAAGAACGCT 318
Db 61 ProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla 80
QY 319 ACTGCTTTCAGGGTAAGTACGCTTCTTGNAGACTTACAACTACACTTTGGGTGCTGAC 378
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QY 499 ATTGCTTCTGCTGAAGGTTTCATTGAGGTTTCCAACTTCGTAAGTTGGTGTGACCCAGGT 558
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QY 1219 GCTTACGTTGAATGATGATGATCAAGCTGAAGAGAACCATTTGGTTAGAGTTTGGTT 1278
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Db 141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160
QY 559 TCTCAACACACCAAGCTTCTCCAGTTATTAACTGATCATTCAGAGGATCGGTAC 618
Db 161 SerGlnProHisGlnAlaSerProValIleAspValIlelleProGluGlySerGlyTyr 180
QY 619 AACAACTTTGGACCAAGCTTCTGCTCTTCCAGACTCTGTAATAGTGGACAC 678
Db 181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200
QY 679 GTTCAGCTTACCTTCACTGCTTCTGCTCCAGCTATTAGAGCTAGATTGGAGCTGAC 738
Db 201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220
QY 739 TTGCGAGGTTACTTTCAGTACGAGAGAGCTTGTACTTATGATGACATGTGCTTC 798
Db 221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240
QY 799 GACACTGTGCTAGAACTTTCAGGCTTACTGAATGTCTCCATTCCTGCTTGTTCAC 858
Db 241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260
QY 859 CACGACCAATGGATCCCAATACGACTTCTGAAAGCTTGGTAGTACTACGGTTACG 918
Db 261 HisAspGluThrArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280
QY 919 GCTGGTAAACCAATGGTCCAGCTCAAGGTTGCTTTCGCTAACGAATGATGTCTAGA 978
Db 281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300
QY 979 TTGACTCAGTCTCAGTTCAGACCCAGCTTCTACTAACACAGCTTTGGAGCTTAACCCA 1058
Db 301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320
QY 1039 GCTACTTCCCATTTGAAGCTTCTTGTAGCTGACTTCTCAGCTTCTCAGCAACACTATGATA 1098
Db 321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340
QY 1099 TCTATTTCTTCGCTTTGGGTTTGTACAAGCGTACCAAGCACTGTCTACTTCTGTGT 1158
Db 341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360
QY 1159 GAATCTATTGAGAACTGACGGTTACTCTGCTTCTTGGACTGTTCATTCGCTGCTAGA 1218
Db 361 GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380
QY 1219 GCTTACGTTGAATGATGCAATGTCAAGCTGAAAGGAACCAITGGTTAGAGTTTTCGTT 1278
Db 381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400
QY 1279 AACGACAGATTGTTCATTCGACGGTTGTGCTGCTTGGAGAGTTGGGTAGATGTAAGA 1338
Db 401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420
QY 1339 GACGACTTCGTTGAAGGTTTCTTCTTCGCTAGATCTGCTGCTGCTGCTGCTGCTGCT 1398
Db 421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGluCysPhe 440
QY 1399 GCT 1401
Db 441 Ala 441

RESULT 4

US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3

; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-2

Alignment Scores:
Pred. No.: 3,03e-222 Length: 467
Score: 2270.00 Matches: 437
Percent Similarity: 90.35% Conservative: 3
Best Local Similarity: 89.73% Mismatches: 7
Query Match: 91.53% Indels: 40
DB: 3 Gaps: 2
US-09-488-265b-28 (1-1404) x US-09-121-425-2 (1-467)

QY 1 ATGGGCGTGTTCGTCTGCTACTGTCCATTCACCTTGTTCGGTTCACATCCGGTACC 60
Db 1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20
QY 61 GCCTTGGGTCTCGTGTAAATTCCTACTCTTGTGACACTGTTGACGCTGGTTACCAATGT 120
Db 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyTyrGlnCys 40
QY 121 TTTCCAGAAATTTCTCACTTGTGGGTACTACTCTCCATCTCTTCTTGGCAGACGAA 180
Db 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
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Db 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla----- 97
QY 301 GCTATTCAAAGAACGCTACTGCTTTCAAGGTAAGTACGCTTCTTGAAGACTTTACAAC 360
Db 98 -----InrTyrAsn 100
QY 361 TACACTTTGGGTGCTCAGCACTTGACTCCATTCGGTGAACCAATGCTTAACCTGCT 420
Db 101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120
QY 421 ATTAAGTCTTACAGAATACAAAGGCTTTGGCTAGAAAGATTGTTCATTTCATTAGAGCT 480
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QY 481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAGTTCAITGAAGCTTTCCAATTCGT 540
Db 141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160
QY 541 AAGTGTGCTGACCCAGGTTCTCAACACACCAAGCTTCTCCAGTTATTAAAC----- 591
Db 161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180
QY 592 -----GTGAATCAT 600
Db 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200
QY 601 CCAGAAGGATCCGGTTACAAACACACTTTGGACCCAGGTTACTTGTACTCTCTTCCGAAGAC 660
Db 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY 661 TCTGAATTAGGTGACGACGCTTGAAGCTAACTTCACTGCTTCTGCTCCAGCTATTAGA 720
Db 221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

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DB 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
QY 781 ATGGACATGTGCCATTGCACACTGCGCTAGAACCTTCTGACGCTACTGAATGTCTCCA 840
DB 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
QY 841 TTCTGTGCTTTGTTCACTCACCAAGATGGATCCCAATACGACTACTTCCAAAGCTTGGGT 900
DB 281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300
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QY 961 AACGAATGATTGCTAGATTGACTCAGCTCCAGTTCAGACCCACACTCTACTAACCAC 1020
DB 321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCCATTTGAACGCTACTTTGTACGCTGACTTCT 1080
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QY 1141 TGTGCTACTACTCTGTTGACTATCTATGAGAACTGACGGTTACTCTGCTCTTGGACT 1200
DB 381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400
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DB 401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGln 420
QY 1261 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCATTTGCACGGTTGCTGTTGACAA 1320
DB 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440
QY 1321 TTGGGTAGATGTAAGAGACGACTCTGGTTGAAGGTTTCTCTTCGCTAGACTCTGGTGT 1380
DB 441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGCTGAATGTTTCGCT 1401
DB 461 AsnTrpAlaGluCysPheAla 467

RESULT 5

US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Leimann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634,493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-634-493A-2

Alignment Scores:
Prod. No.: 3,03e-222 Length: 467
Score: 2270.00 Matches: 437
Percent Similarity: 90.35% Conservative: 3
Best Local Similarity: 89.73% Mismatches: 7
Query Match: 91.53% Indels: 40
Gaps: 2
US-09-488-265B-28 (1-1404) x US-09-634-493A-2 (1-467)
QY 1 ATGGCGCTGTTTCGCTGCTACTCTCCATTGCCACCTTGTTCGGTTCACATCCGGTACC 60
DB 1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20
QY 61 GCCTGGGTCCTCGTGGTAATTCACCTCTGTGTGACACAGTGTGACGGTGGTTACCAATGT 120
DB 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40
QY 121 TTCACAGAAATTTCTCACTTGTGGGTACCTACTCTCCATCTCTCTCTTTGGCAGAGCAA 180
DB 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
QY 181 TCTGCTATTTCTCAGAGGTTCCACAGACTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
DB 61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80
QY 241 AGACACGGTGTAGATACCCAACTTCTTCTCGTCTAAGGCTTACTCTCTGCTTTCATTCAA 300
DB 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla ----- 97
QY 301 GCTATTCAAAAGAAGCTACTCTTCAAGGTAAGTACGCTTCTTGAAGACTTCAAC 360
DB 98 -----ThrTyrAsn 100
QY 361 TACACTTTGGTGTGACGACTTGCATCCATCCGTTGAAACCAATAGTTAACTCTGGT 420
DB 161 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120
QY 421 ATTAAGTCTTACAGAGATACAAGCTTTGGCTAGAAAGATGTTCATTCATTAGAGCT 480
DB 121 IleLysPheTyrAlaArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140
QY 481 TCTGTTCTGACAGAGTTATGCTTCTCTGAAAGTTTCATTGAAGGTTTCCAACTCTGCT 540
DB 141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160
QY 541 AAGTTGGCTGACCCAGGTTCTCAACCCACCAAGCTTCTCCAGTTTATTAAC----- 591
DB 161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180
QY 592 -----GTGATCATT 600
DB 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200
QY 601 CCAGAAGGATCCGGTTACAAACAACACTTTGGACCCAGGTACTTGTACTGCTTTCGAAGAC 660
DB 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY 661 TCTGAATTAGGTGACGAGCTTGAAGCTAACTTCACIGCTTTGTTCGCTCCAGCTATPAGA 720
DB 221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
QY 721 GCTAGATTGGAAGCTGACTTCCAGGTTACTTTCAGTCTGACGAGAGGTTGTTTACTTG 780
DB 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValTyrLeu 260
QY 781 ATGGACATGTGCTCATTCACACTGCTCGCTAGAACTTCTGACGCTACTGAATGTCTCCA 840
DB 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
QY 841 TTCTGTGCTTTTTCACCTCACGACGAATGGATGCCAATACGACTACTTCCAAAGCTTGGGT 900
DB ----- 940

Db	281	PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyraSpTyrLeuGlnSerLeuGly	300
Qy	901	AACTACTACGGTTACGGTCTGGTAACCCATTGGGTCCAGCTCAAGGTGTGGTTTCGGT	960
Db	301	LysTyrTrpGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla	320
Qy	961	AACGAATGATGCTAGATTGACTCACTCTCCAGTTTCAAGACACACACTTCTACTATCCAC	1020
Db	321	AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspIsthrSerThrAsnHis	340
Qy	1021	ACTTTGACTCTAACCCAGCTACTTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCT	1080
Db	341	ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer	360
Qy	1081	CACGACAACACTATGATATCTATTCTTCGCTTTGGGTTTGTACACAGCTACCAAGCCA	1140
Db	361	HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro	380
Qy	1141	TTGCTCTACTCTCTGTGTAATCTATTGAAGAAACTGACGGTACTCTGCTTCTTGCACT	1200
Db	381	LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr	400
Qy	1201	GTTCCTTCCTGCTAGAGCTTACGTTGAATCATCAATGTCAAGCTGAAAAGGAACCA	1260
Db	401	ValProPheClyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro	420
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Qy	1321	TTGGGTAGATGTGAAGACAGACACTCTGTTTGAAGGTTTGTCTTCGTACATCTGTTGGT	1380
Db	441	LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly	460
Qy	1381	AACTGGGCTGAATGTTTCGCT	1401
Db	461	AsnTrpAlaGluCysPheAla	467

RESULT 6

US-07-923-724-8
 ; Sequence 8, Application US/07923724
 ; Patent No. 5780292
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Nevalainen, Helena K.M.
 ; APPLICANT: Paloheimo, Marja T.
 ; APPLICANT: Miettinen-Oinonen, Arja S.K.
 ; APPLICANT: Torkkeli, Tuula K.
 ; APPLICANT: Cantrell, Michael
 ; APPLICANT: Piddington, Christopher S.
 ; APPLICANT: Rambossek, John A.
 ; APPLICANT: Tutunen, Marja K.
 ; APPLICANT: Fagerström, Richard B.
 ;
 ; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
 ; TITLE OF INVENTION: 1a Trichoderma
 ; NUMBER OF SEQUENCES: 66
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Sterre, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ;
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/923,724
 ; FILING DATE: 31 JUL-1992
 ; CLASSIFICATION: 435
 ;
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/496,155

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Db 201 SerGluAlaSerSerAsnThrLeuAspProGlyThrCysThrVal-PheGluAsp 220
Qy 661 TCTGAATTAGTGGAGCGGTGAGCTTAACCTTCTACTGCTTTGCTGCTCCAGCTATTAGA 720
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Qy 721 GCTAGATTGGAAGTGAAGTCTCCAGGCTTACTTTGACTGACGAGAGCTGTTTACTTG 780
Db 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
Qy 781 ATGGACATGTCTCCATTCGACACACTGCTGAGAACTTCTGACGCTACTGAAATGCTCCA 840
Db 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
Qy 841 TCTGCTGCTTGTTCACCTACGACGAGAGTGGATGGAATCAATACGACTACTTCCAAAGCTTGGT 900
Db 281 PheCysAspLeuPheThrHisAspGluTrpIleHisTyrAspThrLeuGlnSerLeuLys 300
Qy 901 AAGTACTACGGTTACGGTGTCTGTAACCCATTGGGTCGACGCTCAAGGTGTGTGGTTCGCT 960
Db 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
Qy 961 AACGAATGATTGCTAGATTGACTACCTCTCCAGTTCACGACACACTTCTACTATAACAC 1020
Db 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 1040
Qy 1021 ACTTGGACTCTAACCCAGCTACTTCCCATTTGACGCTACTTCTACGCTGACGCTCTCT 1080
Db 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
Qy 1081 CACGACACACTATGATATCTATTCTCTCTGCTTTGGGTTTGTACAGGTTACCAAGCCA 1140
Db 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuIleAsnGlyThrLysPro 380
Qy 1141 TTGCTACTACTTCTGTTGATCTATTCAGAACTGACGGTTACTTCTGCTTCTTGGACT 1200
Db 381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaIleThr 400
Qy 1201 GTTCATTGCTGCTAGAGCTTACGTTCAATGATGAATGCAAGTCAAGCTGAAAGCAACCA 1260
Db 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlyPro 420
Qy 1261 TTGCTAGAGTTTGGTTTAACACAGAGTGTCTCCATTGACGCTGTGCTGTGACAAG 1320
Db 421 LeuValArgValLeuValAsnAspArgValValProIleuHisGlyCysProIleAspAla 440
Qy 1321 TTGGGTAGATTAAGACAGACGACTTGGTTCAAGGTTTGTCTTTCGCTAGACTCTGGTGGT 1380
Db 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
Qy 1381 AACTGGGCTGAATGTTTCGT 1401
Db 461 AspTrpAlaGluCysSerAla 467
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RESULT 7

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US-08-609-426A-8
; Sequence 8, Application: US/08609426A
; Patent No. 5830733
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambossek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerström, Richard B.
; APPLICANT: Houston, Christine S.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 69
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Alignment Scores:

Pred. No.:	1-93e-182	Length:	467
Score:	1879.00	Matches:	353
Percent Similarity:	84.37%	Conservative:	41
Best Local Similarity:	75.59%	Mismatches:	73
Query Match:	75.77%	Indels:	0
DB:	2	Gaps:	0

US-09-488-265B-28 (1-1404) x US-08-609-426A-8 (1-467)

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Db	21	AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyThrGlnCys	40
Qy	121	TTCCAGAAATTTCTCCTACTGTGGGTACTCTCTCCATACITCTCTTTGGCAGACGAA	180
Db	41	PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu	60
Qy	181	TCTGCTATTTCTCCACAGACGCTTCCAGACGACTGTAGAGTTACTTCTGCTCAAGTTTGTCT	240
Db	61	SerAlaIleSerProAspValProAlaGlyCysArgValThrPheAlaGlnValLeuSer	80
Qy	241	AGACAGGCTGCTAGATACCACTTCTCTGCTCTAAGGCTTACTCTGCTTGTATTGAA	300
Db	81	ArgHisGlyAlaArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu	100

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Db 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
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QY 541 AGTTGGTGCACCCAGGTTCTCAACACACACAGCTTCTCCAGTTATTAACTGATCAT 600
Db 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200
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Db 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATTAGTGACGACGCTGAAGCTTAACCTCCTGCTTCTCCCTCCAGCTATTAGA 720
Db 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheAlaProSerIleArg 240
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Db 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyLeu 260
QY 781 ATGCACATGTCTCATTGACACTGCTGCTAGAACTTCTGACGCTACTCAATGTCTCCA 840
Db 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
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QY 901 AAGTACTACGGTTACGGTGTGTGTACCCATTCGGTCCAGCTCAAGGTGTGTTTCCGT 960
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QY 961 AACGAATTGATTCTAGATTGACTCACTCTCCAGTTCAAGACACACACTTCTACTACACAC 1020
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QY 1021 ACTTTGACTCTTAACCCAGCTACTTTCCCAITGACGCTACTTTGTACGCTGACTTCTCT 1080
Db 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnSerThrLeuTyAlaAspPheSer 360
QY 1081 CAGCACAACTATGATATCTATTCTTCTGGCTTGGGTTGTACACGGTACCAAGCA 1140
Db 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyArgAsnGlyThrLysPro 380

QY 1141 TTGTCTACTACTTCTGTGTAATCTATTGAAGAACTGACCGTACTTCTGCTTCTGGACT 1200
Db 381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
QY 1201 GTTCCATTGCGTCTAGAGCTTACGTTGAATGATCAATGCTCAAGCTGAAAGGAACCA 1260
Db 401 ValProPheAlaSerArgLeuTyValGluMetMetGlnCysGlnAlaGluGlnGluPro 420
QY 1261 TTGTTAGAGTTTGGTTAAGCAGAGAGTGTTCCTATTGACGCTTGTGCTGTTGACAAG 1320
Db 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProIleAspAla 440
QY 1321 TTGGTACATGTAGAGAGAGAGCTTCTGTTGAAAGCTTGTCTTTCGTAGATCTGGTGT 1380
Db 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGCTGAATGTTCCGCT 1401
Db 461 AspTrpAlaGluCysSerAla 467
RESULT 9
US-08-151-574-32
: Sequence 32, Application US/08151574
: Patent No. 5436156
: GENERAL INFORMATION:
: APPLICANT: Robert F.M. Van Gorpom
: APPLICANT: Willem Van Hartingsveldt
: APPLICANT: Petrus A. Van Paridon
: APPLICANT: Annemarie E. Veenstra
: APPLICANT: Rudolf G.M. Luttin
: APPLICANT: Gerardus Selten
: TITLE OF INVENTION: Cloning and Expression of Microbial
: TITLE OF INVENTION: Phytase
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESS: Morrison & Pocrster
: STREET: 545 Middlefield Road, Suite 200
: CITY: Menlo Park
: STATE: California
: COUNTRY: USA
: ZIP: 94025-3471
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: SOFTWARE:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/151,574
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/688,578
: FILING DATE: 24-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 24615-20026.00
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-327-7250
: INFORMATION FOR SEQ ID NO: 32:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 467 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-151-574-32
Alignment Scores:
Pred. No.: 4.93e-182 Length: 467
Score: 1875.00 Matches: 353
Percent Similarity: 84.37% Conservative: 41

TELEPHONE: 415-813-566

TELEPHONE: 415-813-566

TELEFAX: 415-494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: signal sequence
 LOCATION: 1...23
 OTHER INFORMATION:
 US-08-693-709-2

Alignment Scores:
 Pred. No.: 4,93e-162 Length: 467
 Score: 1875.00 Matches: 353
 Percent Similarity: 84.37% Conservative: 41
 Best Local Similarity: 75.59% Mismatches: 73
 Query Match: 75.60% Indels: 0
 DB: 1 Gaps: 0

US-09-488-265B-28 (i-1404) x US-08-693-709-2 (1-467)

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DB 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TCCACAGAAATTTCTACITCTGCGGTACCTCTCCATCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 41 PheSerGlnThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
QY 181 TCTGCTATTCTCCAGACGTTCCAGACGCTGTAGAGTACTTCTGTTCAAGTTTGTCT 240
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QY 361 TACACTTGGGTGCTGACGACTTCACTCCATTCGGTGAACCAATATGTTTACTCTGCT 420
DB 121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGlnGlnGluLeuValAsnSerGly 140
QY 421 ATTAAGTTCTACAGAATACAAAGCTTTCGCTAGAAAGATTGTTCCATTCTATAGACT 480
DB 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 481 TCTGTTCTGACAGAGTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 161 SerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSerThr 180
QY 541 AGITGGGTGACCAAGTCTTCACACCAACCACTTCCTCCAGTTCCTCCAGTTCCTCCAG 600
DB 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerProLysIleAspValIle 200
QY 601 CAGAAGGATCCGGTTACAAACAACTTTGACCAACGACTTCTGCTGCTTTCGAAGAC 660
DB 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATTAGGTGACGAGCTTGAAGCTAACTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

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DB 241 GlnArgLeuGlnAsnAspLeuSerGlyValThrLeuThrAspThrGlyValThrTyrLeu 260
QY 781 ATGGACATGTGTCCATTCGACACACTCTCGTCAAACTTCTGACGCTACTGAATCTCTCCA 840
DB 261 MetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSerPro 280
QY 841 TTCTGTGCTTGTTCCTCCTCAGCAGCAATGGATCCAAATACGACTACTTCCAAAGCTTGGT 900
DB 281 PheCysAspLeuPheThrHisAspGlnTyrPheAsnTyrAspTyrLeuGlnSerLeuLys 300
QY 901 AAGTACTACGGTACGGTAAACCATTTGGTCCAGCTCAAGGTGTTGGTTGCT 960
DB 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY 961 AACGAATTGATGTAGATTGACTCACTCTCCAGTTCAGACCACTCTCTACTTCTACTAAC 1020
DB 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340
QY 1021 ACTTTGGACTCTAACCCACCTACTTCCCATTCGAACGCTACTTGTACGCTGACTTCTCT 1080
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QY 1081 CACGACACACTATCATATCTATTTCTTCTGCTTGGGTTTGTACAAAGCTACCAAGCCA 1140
DB 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
QY 1141 TTGCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTACTCTGCTTCTTGGACT 1200
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DB 401 ValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGluGlnGluPro 420
QY 1261 TTGGTTAGAGTTTGGTTAAGCAGACAGTTGTTCCATTGACAGGTTGCTGTTGACAAG 1320
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QY 1321 TTGGGTAGATGTAAAGACGACGACTTCTGTTAGAGTTTCTCTTCGCTAGATCTGTTGGT 1380
DB 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AAATGGGCTGAATGTTTGGCT 1401
DB 461 AspTyrAlaGluCysPheAla 467

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RESULTS

CS-08-419-448-32
 Sequence 32, Application US/08419448
 Patent No. 5863533
 GENERAL INFORMATION:
 APPLICANT: Robert F.M. Van Gorkom
 APPLICANT: Willem Van Hartingsveldt
 APPLICANT: Petrus A. Van Paridon
 APPLICANT: Annemarie E. Veenstra
 APPLICANT: Rudolf G.M. Luttin
 APPLICANT: Gerardus Selten
 TITLE OF INVENTION: Cloning and Expression of Microbial
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morisson & Foerster
 STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006-1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-819-825-3

Alignment Scores:

Pred. No.: 4,93e-182 Length: 467
Score: 1875.00 Matches: 353
Percent Similarity: 84.37% Conservative: 41
Best Local Similarity: 75.59% Mismatches: 73
Query Match: 75.60% Indels: 0
DB: 2 Gaps: 0

US-09-488-265b-28 (1-1404) x US-08-819-825-3 (1-467)

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QY 61 GCCTGGGTCCTCGTGGTAAATTCCTCAGCTTGTGACACTGTGTGACGGTGGTTACCAATGI 120
DB 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

QY 121 TTCCCAAGAATTCACACTTGGGGTACTCTCCATCTCTGCTAAGCTTACTCTGCTTGGCAGAGAA 180
DB 41 PheSerGluThrSerHisLeuThrGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

QY 181 TCTGCTATTCTCCAGACGCTCCACAGCACTAGAGTTACTTTCGTTCAAGTTTGTCT 240
DB 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

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DB 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrAlaPheLeuLysThrTyrAsn 100

QY 301 GCTATTCAAAGAAGCGTACTGCTTTCAAGGTAAGTACGCTTCTTGAAGACTTACAAAC 360
DB 101 GluIleGlnAlaSerAlaThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

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DB 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

QY 481 TCTGGTTCTGACAGACTTATTGCTTCTGCTGAAAAGTTCAITGAAGGTTTCCAATCTGCT 540
DB 161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

QY 541 AAGTTGGCTGACCGGTTCTCAACACACACCAAGCTTCTCCAGTTATTAACTGATCAT 600
DB 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerProLysIleAspValIle 200
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QY 661 TCTGAATAGGTGACGACGCTGAAGCTAACTTCACCTGCTTGTTCGGTCCAGCTATTAGA 720
DB 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 721 GCTAGATTGGAAGCTGACTGCCAGGTGTACTTGTGACTGACGAGAGGTTGTTACTTG 760
DB 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
QY 781 ATGGACATGTGTCCATTCGACACTCTCGCTAGAACTCTGACGCTACTGAATGCTGCCA 840
DB 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
QY 841 TTCTGTGCTTTCTTCCACTCAGCAGCAATGATCCAAATACGACTACTTGCAGAGTGGGI 900
DB 281 PheCysAspLeuPheThrHisAspGluTyrPheAsnTyrAspTyrLeuGlnSerLeuLys 300
QY 901 AAGTACTAGGTACGGTCTGCTGTAACCCATTCGGTCCAGCTCAAGGTTGGTTCGCT 960
DB 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY 961 AACGAATTGATTGCTAGATTGACTCCTCCTCAGTTCAAGACCACTTCTTACTAACCA 1020
DB 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340
QY 1021 ACTTGGACICTAACCCAGCTACTTTCCTCATTGAACGCTACTTGTAGCTGCTCTCTCT 1080
DB 341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
QY 1081 CAGCAACAACATATGATATCTATTTCTTCGTTTGGTGGTTCACACGGTACCAAGCCA 1140
DB 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
QY 1141 TTGCTACTACTTCTGTTGAATCTATTGAAGAACTACGGTTACTCTGCTTCTTGGACT 1200
DB 381 LeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyrThr 400
QY 1201 GTTCCATTTCGCTAGAGCTTACGTTGAATGATGCAATGTCAGCTGCAAGCTGAAAGAACCA 1260
DB 401 ValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGlnGlnGluPro 420
QY 1261 TTGGTTAGAGTTTGGCTTAACGACAGAGTTGTCCATTGACGGTTGTGCTGTGACAA 1320
DB 421 LeuValArgValLeuValAsnAspArgValProLeuHisGlyCysProValAspAla 440
QY 1321 TTGGGTAGATGTAAAGAGACGACCTTCGTTGAAGTTTGTGCTTTCGCTAGACTCTGCTGT 1380
DB 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGCTGAATGTTTCGCT 1401
DB 461 AspTyrAlaGluCysPheAla 467
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RESULT 14

US-09-163-642-3

Sequence 3, Application US/09163642

Patent No. 6221644

GENERAL INFORMATION:

APPLICANT: Berk, Randy M.

APPLICANT: Ray, Michael W.

APPLICANT: Klotz, Alan V.

TITLE OF INVENTION: Polypeptides Having Phytase Activity

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6221644 of No. 6221644th America, Inc.

STREET: 405 Lexington Avenue, Suite 6400

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/163,642
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1987
ATTORNEY/AGENT INFORMATION:
NAME: Landiris, Elias J.
REGISTRATION NUMBER: 33,728
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-163-642-3

Alignment Scores:
Pred. No.: 4,33e-182 Length: 467
Score: 1875.00 Matches: 353
Percent Similarity: 84.37% Conservative: 41
Best Local Similarity: 75.59% Mismatches: 73
Query Match: 75.60% Indels: 0
DB: 3 Gaps: 0

US-09-488-265B-28 (1-1404) x US-09-163-642-3 (1-467)

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QY 61 GCCTTGGTGCTCGTGGTAATCTCACTCTGTGACACTGTGTGACGGTGGTACCAATCT 120
DB 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TTCACCAAAATTTCTCACTTGTGGGTACCTACTCTCCATCTCTCTTTGGCAGACGAA 180
DB 41 PheSerGluThrSerHisLeuTyrPglyGlnTyrrAlaProPhePheSerLeuAlaAsnGlu 60
QY 161 TCTGCTATTTCTCCAGACGCTCCAGACGACTGTAGAGTTACTTTCTGCTTCAAGTTTGTCT 240
DB 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY 241 AGACACGGTCTAGATACCAACTCTCTCTGCGCTCTAAGCTTACTCTGCTTTGATTGAA 300
DB 81 ArgHisGlyAlaArgTyrProThrAspSerLeuGlyLysTyrSerAlaLeuIleGlu 100
QY 301 GCTATTTCAAAGAACGCTACTGCTTTCAAGGTAAAGTACGCTTTCTTGAAGACTTACAAC 360
DB 101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTTGGTGTGACGACTGTACTCCATTCGGTGAACCAAAATGTTAACTCTGTGT 420
DB 121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAAGTTCTACAGACATACAGGCTTTGGCTAGAAAGATTTCTTCATTCATTTAGAGT 480
DB 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
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RESULT 15

US-09-233-310-32
; Sequence 32, Application US/09233510
; Patent No. 6350602
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorkom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seltin
; TITLE OF INVENTION: Cloning and Expression of Microbial

Search completed: October 3, 2003, 08:57:09
Job time : 45.0567 secs

GenCore version: 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:45 ; Search time 12.1257 Seconds
(without alignments)
1524.850 Million cell updates/sec

Title: US-09-488-265B-27
Perfect score: 2321
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs. 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cqn2_6/ptodata/1/iaa/6A_COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1902	81.9	467	3	US-09-121-425-2
5	1902	81.9	467	4	US-09-634-493A-2
6	1762.5	75.9	439	4	US-09-044-718-3
7	1762.5	75.9	449	4	US-09-044-718-12
8	1762.5	75.9	465	3	US-08-868-435-33
9	1762.5	75.9	465	4	US-08-744-231-33
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25	1684	72.6	467	1	US-08-693-709-2
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27	1684	72.6	467	2	US-08-819-825-3

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40	1672	72.0	467	4	US-09-273-871A-11	Sequence 11, Appli
41	1672	72.0	467	4	US-09-929-060-3	Sequence 3, Appli
42	1667	71.8	443	3	US-09-155-855-2	Sequence 2, Appli
43	1667	71.8	443	4	US-09-543-744-2	Sequence 2, Appli
44	1667	71.8	443	4	US-09-929-060-2	Sequence 2, Appli
45	1660	71.5	462	4	US-09-636-499-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-09-121-425-1
: Sequence 1, Application US/09121425
: Patent No. 6153418
: GENERAL INFORMATION:
: APPLICANT: Lehmann, Martin
: TITLE OF INVENTION: Consensus Phytases
: FILE REFERENCE: Consensus phytases 13239
: CURRENT APPLICATION NUMBER: US/09/121.425
: CURRENT FILING DATE: 1998-07-23
: EARLIER APPLICATION NUMBER: EPO 97112688.3
: EARLIER FILING DATE: 1997-07-24
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patent Ver. 2.0
: SEQ ID NO 1
: LENGTH: 441
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:consensus
: OTHER INFORMATION: sequence
US-09-121-425-1

Query Match	87.0%	Score	2020	DB	3	Length	441
Rest. Local Similarity	89.3%	Pred. No.	3.1e-207				
Matches	430	Conservative	10	Mismatches	20	Indels	18
Gaps	10						
QY	1	NSHSCDTVD-GYQC-PEISHLWGQYSPFSLADESAISPDVPGCRVTFFVQVLSRHGARY	58				
DB	1	NSHSCDTVGGYQCPEISHLWGQYSPFSLADESAISPDVPGCRVTFFVQVLSRHGARY	60				
QY	59	PTSSKSKYSALIERIQKNAT-FKGYAFELKTYNTLTGADDLTPEGNQMVNSGIFKYYR	117				
DB	61	PTSSKSKYSALIEAIQKNATAPFKGYAFELKTYNTLTGADDLTPEGNQMVNSGIFKYYR	120				
QY	118	YKALARNIYVFRASCSDRVIASAEKFTGFSQAKLADPA---HQASPINVIIEGSGY	174				
DB	121	YKALARKIYVFRASCSDRVIASAEKFTGFSQAKLADPGSQPHOASPIDVIEGSGY	180				
QY	175	NNTLDHGLCTAFEDSTGLGDGAENFATVFAPIRARLEA-LPGVNLTDDEVVNLMDMCPF	233				
DB	181	NNTLDHGLCTAFEDSELGDGVANFTALFAPIRARLEADLPGVTLTDEDVYVYLMDCPF	240				
QY	234	DTVARTSDATQLSPFCDLFTADEW-QYDYQLSL-KYGYGAGNPLGPAQGVCF-NELIAR	290				
DB	241	ETVARTSDATQLSPFCDLFTADEW-QYDYQLSL-KYGYGAGNPLGPAQGVCF-NELIAR	300				
QY	291	LTHSPVDHTSTNHTLDSNPATFFPLNATLYADFSHDNTWMSIFFALGLYNGTKPLSTTSV	350				
DB	301	LTRSPVDHTSTNHTLDSNPATFFPLNATLYADFSHDNTWMSIFFALGLYNGTKPLSTTSV	360				

QY 351 EST-ETDGYAASWTVPFAARAYVEMMOCEAGGGGEGEKEPLVRVLVNDVRVPLHGGGVD 409
Db 361 ESIEETDGYASWTVPFGARAYVEMMOCA-----EKEPLVRVLVNDVRVPLHGGCAVD 413
QY 410 KLGRCKLDDFVEGLSFARSGGNWAECEFA 437
Db 414 KLGRCKRDDFVEGLSFARSGGNWAECEFA 441

RESULT 2

US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273.871A
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080.129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090.675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version. 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-634-493A-1

Query Match 87.0%; Score 2020; DB 4; Length 441;
Best Local Similarity 89.3%; Pred. No. 3.4e-207;
Matches 400; Conservative 10; Mismatches 20; Indels 18; Gaps 10;
QY 1 NSHSCDVTVD-GYQC-PEISHLWGOYSPFFSLADESALSPDPKGRVTFVQVLSRHGARY 58
Db 1 NSHSCDVTVDGGYQCFPEISHLWGOYSPFFSLEDESALSPDPDCRVTFVQVLSRHGARY 60
QY 59 PTSSKSKYSALIERIOKNAT-FKGKYAFKTYNTILGADDLTPFGENQMVNSGKIFYRR 177
Db 61 PTSSKSKYSALIEAIOKNATAFKGYAFKTYNTILGADDLTPFGENQMVNSGKIFYRR 120
QY 118 YKALARNIVPVRASGSDRVIASAEKFTGFSQAKLADPA---HQASPVINVIIPEGSGY 174
Db 121 YKALARKIVPPIRASGSDRVIASAEKFTGFSQAKLADPGSQPHQASPVIDVIIPEGSGY 180
QY 175 NNTLDHGLCTAFEDSTLGDDEANFTAVFAPPFIRARLEA-LPGVNLTDDEVNLMDCPF 233
Db 181 NNTLDHGLCTAFEDSELGDDEANFTALFAPAIRARLEADLPVTLTDEDVYVLMDCPF 240
QY 234 DTVARTSDATQSLSPCDLFTADEW-QYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
Db 241 ETVARTSDATELSPPCALFTHDEWQDYLOSLKYYGYGAGNPLGPAQGVGFANELIAR 300
QY 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFPFGALGYNGTAPLSTTSV 350
Db 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFPFGALGYNGTAPLSTTSV 360
QY 351 EST-ETDGYAASWTVPFAARAYVEMMOCEAGGGGEGEKEPLVRVLVNDVRVPLHGGGVD 409
Db 361 ESIEETDGYASWTVPFGARAYVEMMOCA-----EKEPLVRVLVNDVRVPLHGGCAVD 413
QY 410 KLGRCKLDDFVEGLSFARSGGNWAECEFA 437
Db 414 KLGRCKRDDFVEGLSFARSGGNWAECEFA 441

RESULT 3

US-09-273-871A-9
; Sequence 9, Application US/09273871-A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273.871A
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080.129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090.675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version. 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Query Match 87.0%; Score 2020; DB 4; Length 467;
Best Local Similarity 89.3%; Pred. No. 3.4e-207;
Matches 400; Conservative 10; Mismatches 20; Indels 18; Gaps 10;
QY 1 NSHSCDVTVD-GYQC-PEISHLWGOYSPFFSLADESALSPDPKGRVTFVQVLSRHGARY 58
Db 27 NSHSCDVTVDGGYQCFPEISHLWGOYSPFFSLEDESALSPDPDCRVTFVQVLSRHGARY 86
QY 59 PTSSKSKYSALIERIOKNAT-FKGKYAFKTYNTILGADDLTPFGENQMVNSGKIFYRR 117
Db 87 PTSSKSKYSALIEAIOKNATAFKGYAFKTYNTILGADDLTPFGENQMVNSGKIFYRR 146
QY 118 YKALARNIVPVRASGSDRVIASAEKFTGFSQAKLADPA---HQASPVINVIIPEGSGY 174
Db 147 YKALARKIVPPIRASGSDRVIASAEKFTGFSQAKLADPGSQPHQASPVIDVIIPEGSGY 206
QY 175 NNTLDHGLCTAFEDSTLGDDEANFTAVFAPPFIRARLEA-LPGVNLTDDEVNLMDCPF 233
Db 207 NNTLDHGLCTAFEDSELGDDEANFTALFAPAIRARLEADLPVTLTDEDVYVLMDCPF 266
QY 234 DTVARTSDATQSLSPCDLFTADEW-QYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
Db 267 ETVARTSDATELSPPCALFTHDEWQDYLOSLKYYGYGAGNPLGPAQGVGFANELIAR 326
QY 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFPFGALGYNGTAPLSTTSV 350
Db 327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFPFGALGYNGTAPLSTTSV 386
QY 351 EST-ETDGYAASWTVPFAARAYVEMMOCEAGGGGEGEKEPLVRVLVNDVRVPLHGGGVD 409
Db 387 ESIEETDGYASWTVPFGARAYVEMMOCA-----EKEPLVRVLVNDVRVPLHGGCAVD 439
QY 410 KLGRCKLDDFVEGLSFARSGGNWAECEFA 437
Db 440 KLGRCKRDDFVEGLSFARSGGNWAECEFA 467

RESULT 4

US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:

QY 2 SHSCDVTVD-GYOC-PEISHLNGQYSPFFSLADESAISPDPVKGRVTFVOVLSRHGARYP 59
1 SKSCDVTDLGQYOCSPATSHLMGQYSPFFSLADESAISPDPVKGRVTFVOVLSRHGARYP 60
QY 60 TSSKSKKYSALLERIQKAT-FKGYAFKLTNTYTLGADDLTPFGENOMVNSGKIFKRYR 116
Db 61 TSSKSKKYSALLERIQKAT-FKGYAFKLTNTYTLGADDLTPFGENOMVNSGKIFKRYR 120
QY 119 KALARNIPVFPVRSASDRVIAAEKFIKGFOSAKLADP--AHQASPVINVIIPGSGYNN 176
Db 121 KALARNIPVFPVRSASDRVIAAEKFIKGFOSAKLADP--AHQASPVINVIIPGSGYNN 180
QY 177 TLHGCLCTAFEDSTLGDAAENFTAVFAPPFIRARLEA-LPGVNLITDEDVYNLMDMCPEDT 235
Db 181 TLHGVCCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVYNLMDMCPEDT 240
QY 236 VARTSDATQSPFCDLFTADEW-OYDYLQSL-KYGYGAGNPLGPAQGVGF-NELIARLT 292
Db 241 VARTSDASQLSPFCDLFTADEW-OYDYLQSL-KYGYGAGNPLGPAQGVGF-NELIARLT 300
QY 293 HSPVODHTSTNHTLDSNPATFPLNATLYADFSHONTMVSIFFFALGLYNGTKPLSTTSVES 352
Db 301 RSPVODHTSTNHTLDSNPATFPLNATLYADFSHONTMVSIFFFALGLYNGTKPLSTTSVES 360
QY 353 I-ETDGYAASVTVPFAARAYVENMOCAGGGGEGEKEPELVRLVNDRVVPLHGCGVDKL 411
Db 361 AKELDGYASWVVPFGARAYFEIMOCKS-----EKEPLVRLVNDRVVPLHGCGVDKL 413
QY 412 GRCKLDDFVEGLSPARSGGNWAECEFA 437
Db 414 GRCKLNDVFVKGLSWARSGGNWGECEFS 439

RESULT 7

US-09-044-718-12
: Sequence 12, Application US/09044718
: Patent No. 6391505
: GENERAL INFORMATION:
: APPLICANT: KOSTREMA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 12
: LENGTH: 449
: TYPE: PRI
: ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Query Match 75.9% Score 1762.5; DR 4; Length 449;
Best Local Similarity 77.4%; Pred. NO. 1.le-179;
Matches 345; Conservative 36; Mismatches 48; Indels 17; Gaps 10;

QY 2 SHSCDVTVD-GYOC-PEISHLNGQYSPFFSLADESAISPDPVKGRVTFVOVLSRHGARYP 59
Db 11 SKSCDVTDLGQYOCSPATSHLMGQYSPFFSLADESAISPDPVKGRVTFVOVLSRHGARYP 70
QY 60 TSSKSKKYSALLERIQKAT-FKGYAFKLTNTYTLGADDLTPFGENOMVNSGKIFKRYR 118
Db 71 TSSKSKKYSALLERIQKAT-FKGYAFKLTNTYTLGADDLTPFGENOMVNSGKIFKRYR 130
QY 119 KALARNIPVFPVRSASDRVIAAEKFIKGFOSAKLADP--AHQASPVINVIIPGSGYNN 176
Db 131 KALARNIPVFPVRSASDRVIAAEKFIKGFOSAKLADP--AHQASPVINVIIPGSGYNN 190

QY 177 TLHGCLCTAFEDSTLGDAAENFTAVFAPPFIRARLEA-LPGVNLITDEDVYNLMDMCPEDT 235
Db 191 TLHGVCCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVYNLMDMCPEDT 250
QY 236 VARTSDATQSPFCDLFTADEW-OYDYLQSL-KYGYGAGNPLGPAQGVGF-NELIARLT 292
Db 251 VARTSDASQLSPFCDLFTADEW-OYDYLQSL-KYGYGAGNPLGPAQGVGF-NELIARLT 310
QY 293 HSPVODHTSTNHTLDSNPATFPLNATLYADFSHONTMVSIFFFALGLYNGTKPLSTTSVES 352
Db 311 RSPVODHTSTNHTLDSNPATFPLNATLYADFSHONTMVSIFFFALGLYNGTKPLSTTSVES 370
QY 353 I-ETDGYAASVTVPFAARAYVENMOCAGGGGEGEKEPELVRLVNDRVVPLHGCGVDKL 411
Db 371 AKELDGYASWVVPFGARAYFEIMOCKS-----EKEPLVRLVNDRVVPLHGCGVDKL 423
QY 412 GRCKLDDFVEGLSPARSGGNWAECEFA 437
Db 424 GRCKLNDVFVKGLSWARSGGNWGECEFS 449

RESULT 8

US-08-868-435-33
: Sequence 33, Application US/08868435
: Patent No. 6291221
: GENERAL INFORMATION:
: APPLICANT: Van Loon, Adolphus
: APPLICANT: Mitchell, David
: TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hoffmann-La Roche Inc.
: STREET: 340 Kingsland Street
: CITY: Nutley
: STATE: New Jersey
: COUNTRY: United States of America
: ZIP: 07110
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/868.435
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/744,231
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Kass, Alan P
: REGISTRATION NUMBER: 32142
: REFERENCE/DOCKET NUMBER: Case Docket 9339
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201) 235-4205
: TELEFAX: (201) 235-2363
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 465 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 104
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 119
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature

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; LOCATION: 205
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 228
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 337
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 374
; OTHER INFORMATION: /note="potential N-glycosylation site"
; US-08-868-435-33

Query Match 75.9%; Score 1762.5; DB 3; Length 465;
Best Local Similarity 77.4%; Pred. No. 1.2e-179;
Matches 345; Conservative 36; Mismatches 48; Indels 17; Gaps 10;

QY 2 SHSCDVID-GYOC-PEISHLWQYSPFFSLADESAISDVDPKGCRTFVQVLSRHGARYP 59
DB 27 SKSCDVIDLGQYOCSPATSHLWQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86
QY 60 TSSKSKKYSALIERIOKNAT-FKGKYAFKTYNTLGCADDLTDPFGENQMVNSGKIFYRY 118
DB 87 TSSKSKKYLKLTVAQANATDFGKFAFLKTYNTLGCADDLTDPFGEOQVNSGKIFYQRY 146
QY 119 KALARNIVPVRASGSDRVIASAEKIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
DB 147 KALARSVVPFIRASGSDRVIASGKIEGFQOAKLADPGATNRAAPASIVIPESSEFNN 206
QY 177 TLHGCLCTAFEDSTLGDAAENFTAVFAPPFIRARLEA-LPGVNLTDDEVDVNLMDMCPDT 235
DB 207 TLHGVCCTKEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFT 266
QY 236 VARTSDATOLSPFCDLFTADEW-QYDYLQSL-KYGYGAGNPLGPAQGVGF-NELIARLT 292
DB 267 VARTSDASQLSPFCQLFTHNEWKYNYLQSLGKYGYGAGNPLGPAQGVGF-NELIARLT 326
QY 293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTWVSIFFALGLYNGTKPLSTTSVES 352
DB 327 RSPVQDHTSTNHTLDSNPATFPLNATMYVDFSDHNSMVSIFFALGLYNGTEPLSTTSVES 386
QY 353 I-ETDGVAAWVVPFAARAVENMOCCEAGSGGGEKEPLVRLVNDVRVPLHGCGVDKL 411
DB 387 AKELDGYSASWVVPFGARAFETWOCKS-----EKEPLVRALINDRVVPLRGCDVDKL 439
QY 412 GRCKLDDFVEGLSFARSGGNWAECEFA 437
DB 440 GRCKLNDFVKGLSWARSGGNWGECS 465

RESULT 9
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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Db 327 RSPVDHTSTNSTLVSNPATFPPLNATMYVDFSHDMSWVSIFFALGLYNGTEPLSRSTSVES 386
Qy 353 I-ETDGYAASWTVPFAARAYVENMOCAGGGGEGEKEPLRVLVNDRVPLHGGGVOKL 411
Db 387 AKELDGYASWVVPFGARAYFETMOCKS-----EKEPLVRALINDRVVPLHGGGVOKL 439
Qy 412 GRCKLDDFVEGLSFARSGGNWAECEFA 437
Db 440 GRCKLNDVFVGLSWARSGGNWGECEFS 465

RESULT 10
US-09-044-718-78
; Sequence 78, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREMA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-78

Query Match 75.9%; Score 1762.5; DB 4; Length 465;
Best Local Similarity 77.4%; Pred. No. 1.2e-179;
Matches 345; Conservative 36; Mismatches 48; Indels 17; Gaps 10;

Qy 2 SHSCDTVD-GYQC-PEISHLWGOYSPFFSLADESALSPDVPKGCRTVTFVQVLSRHGARYP 59
Db 27 SKSCDTVDLGYQCSPATSHLWGOYSPFFSLEDELSVSSKLKPKDCRITLVQVLSRHGARYP 86
Qy 60 TSSKSKYKALIERIOKNAT-FKGKYAFILKTYNTILGADDLTPFGENQMVNSGIRFYRY 118
Db 87 TSSKSKYKLVTAIQANATDFKGFAPLKYNTYILGADDLTPFGEQQLVNSGIRFYRY 146
Qy 119 KALARNIVPVRASGSDRVIASAEKTEGFQSAKLADP--AHQASPVINVIPEGSYNN 176
Db 147 KALARSVPFIRASGSDRVIASGEKTEGFQQAQAKLADPGATNRAAPASVPIPESEIFNN 206
Qy 177 TLDHGLCTAFEDSLGDAAEFANFTAVFAPPIRARLEA-LPGVNLTDDEVVNLMDMCPPT 235
Db 207 TLDHGVTCKEASQLGDEVAENFTALFADIRARAELHPLGVTLTDEDVVSLMDMCSFT 266
Qy 236 VARTSDATQLSPFCDLTADW-OYDYLOSL-KYGYGAGNPLGPAQGVCF-NELIARLT 292
Db 267 VARTSDASQLSPFCOLTFTHNEWKYNTLQSLKYGYGAGNPLGPAQGGIGFTNELIARLT 326
Qy 293 HSPVDHTSTNHTLDSNPATFPPLNATMYVDFSHDMSWVSIFFALGLYNGTEPLSRSTSVES 352
Db 327 RSPVDHTSTNSTLVSNPATFPPLNATMYVDFSHDMSWVSIFFALGLYNGTEPLSRSTSVES 386
Qy 353 I-ETDGYAASWTVPFAARAYVENMOCAGGGGEGEKEPLRVLVNDRVPLHGGGVOKL 411
Db 387 AKELDGYASWVVPFGARAYFETMOCKS-----EKEPLVRALINDRVVPLHGGGVOKL 439
Qy 412 GRCKLDDFVEGLSFARSGGNWAECEFA 437
Db 440 GRCKLNDVFVGLSWARSGGNWGECEFS 465

RESULT 12
US-09-273-871A-8
; Sequence 8, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618,500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
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RESULT 11
US-09-636-499-6
; Sequence 6, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC886-2
; CURRENT APPLICATION NUMBER: US/09/636,499
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,960
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-636-499-6

Query Match 75.9%; Score 1762.5; DB 4; Length 465;
Best Local Similarity 77.4%; Pred. No. 1.2e-179;
Matches 345; Conservative 36; Mismatches 48; Indels 17; Gaps 10;

Qy 2 SHSCDTVD-GYQC-PEISHLWGOYSPFFSLADESALSPDVPKGCRTVTFVQVLSRHGARYP 59
Db 27 SKSCDTVDLGYQCSPATSHLWGOYSPFFSLEDELSVSSKLKPKDCRITLVQVLSRHGARYP 86
Qy 60 TSSKSKYKALIERIOKNAT-FKGKYAFILKTYNTILGADDLTPFGENQMVNSGIRFYRY 118
Db 87 TSSKSKYKLVTAIQANATDFKGFAPLKYNTYILGADDLTPFGEQQLVNSGIRFYRY 146
Qy 119 KALARNIVPVRASGSDRVIASAEKTEGFQSAKLADP--AHQASPVINVIPEGSYNN 176
Db 147 KALARSVPFIRASGSDRVIASGEKTEGFQQAQAKLADPGATNRAAPASVPIPESEIFNN 206
Qy 177 TLDHGLCTAFEDSLGDAAEFANFTAVFAPPIRARLEA-LPGVNLTDDEVVNLMDMCPPT 235
Db 207 TLDHGVTCKEASQLGDEVAENFTALFADIRARAELHPLGVTLTDEDVVSLMDMCSFT 266
Qy 236 VARTSDATQLSPFCDLTADW-OYDYLOSL-KYGYGAGNPLGPAQGVCF-NELIARLT 292
Db 267 VARTSDASQLSPFCOLTFTHNEWKYNTLQSLKYGYGAGNPLGPAQGGIGFTNELIARLT 326
Qy 293 HSPVDHTSTNHTLDSNPATFPPLNATMYVDFSHDMSWVSIFFALGLYNGTEPLSRSTSVES 352
Db 327 RSPVDHTSTNSTLVSNPATFPPLNATMYVDFSHDMSWVSIFFALGLYNGTEPLSRSTSVES 386
Qy 353 I-ETDGYAASWTVPFAARAYVENMOCAGGGGEGEKEPLRVLVNDRVPLHGGGVOKL 411
Db 387 AKELDGYASWVVPFGARAYFETMOCKS-----EKEPLVRALINDRVVPLHGGGVOKL 439
Qy 412 GRCKLDDFVEGLSFARSGGNWAECEFA 437
Db 440 GRCKLNDVFVGLSWARSGGNWGECEFS 465
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Db 27 SKSCDVTDLGYQCSPTAHLWGQYSPFFSLEDELVSXKLPKDCRIILVQLSRHGARYP 86
Qy 60 TSSKSKYKYSALIERIQKNAT-FKGKYAFLLKTYNYTLGADDLTPFGENOMVNSGKIFRYRY 118
Db 87 TSSKSKYKYLVTAIQANATDFKGFAPLKYNYTLGADDLTPFGEOQLVNSGKIFRYQY 146
Qy 119 KALARNIVPVRASGSDRVIASAEKFTIEGQFQAKLADPGATNRAAPASIVIIPESETEFN 176
Db 147 KALARSVVPFIRASGSDRVIASAEKFTIEGQFQAKLADPGATNRAAPASIVIIPESETEFN 206
Qy 177 TLDHGLCTAFEDSTLGDADAEANFTAVFAPPFIRARLEA-LPGVNLTDDEVDVNLMDMCPDPT 235
Db 207 TLDHGVCTKFEASOLGDEVAANFTALFAPDIRARAKHLPGVLTDEVDVSLMDMCSFDI 266
Qy 236 VARTSDATQSPFCDLFTADEW-OYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
Db 267 VARTSDASOLSPPCOLFTHNEWKKNYLOSLGKYGYGAGNPLGPAQGVGF-NELIARLT 326
Qy 293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFFALGLYNGTKPLSTTSVES 352
Db 327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDMSWVSIFFALGLYNGTEGLSRTSVES 386
Qy 353 I-ETDGYAASWTVPFAARAYVENMOCAGGGGEGEKEPLVRVLVNDRVVPLHGGGVDKL 411
Db 387 AKELDGYASASWVVPFGARAYFETMCKS-----EKEPLVRALINDRVVPLHGGGVDKL 439
Qy 412 GRCKLDDFVGLSFAKSGGNWAECPA 437
Db 440 GRCKLNDFVKLSWARSGGNMGECFS 465
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RESULT 15

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US-09-044-718-81
; Sequence 81, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044.718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-81
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Query Match 75.4%; Score 1750.5; DB 4; Length 465;
Best Local Similarity 76.9%; Pred. No. 2.3e-178;
Matches 343; Conservative 37; Mismatches 49; Indels 17; Gaps 10;
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Qy 2 SHSCDVTVD-GYQC-PEISHLWGQYSPFFSLEDELVSXKLPKDCRIILVQLSRHGARYP 59
Db 27 SKSCDVTDLGYQCSPTAHLWGQYSPFFSLEDELVSXKLPKDCRIILVQLSRHGARYP 86
Qy 60 TSSKSKYKYSALIERIQKNAT-FKGKYAFLLKTYNYTLGADDLTPFGENOMVNSGKIFRYRY 118
Db 87 TSSKSKYKYLVTAIQANATDFKGFAPLKYNYTLGADDLTPFGEOQLVNSGKIFRYQY 146
Qy 119 KALARNIVPVRASGSDRVIASAEKFTIEGQFQAKLADPGATNRAAPASIVIIPESETEFN 176
Db 147 KALARSVVPFIRASGSDRVIASAEKFTIEGQFQAKLADPGATNRAAPASIVIIPESETEFN 206
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Qy 177 TLDHGLCTAFEDSTLGDADAEANFTAVFAPPFIRARLEA-LPGVNLTDDEVDVNLMDMCPDPT 235
Db 207 TLDHGVCTKFEASOLGDEVAANFTALFAPDIRARAKHLPGVLTDEVDVSLMDMCSFDI 266
Qy 236 VARTSDATQSPFCDLFTADEW-OYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
Db 267 VARTSDASOLSPPCOLFTHNEWKKNYLOSLGKYGYGAGNPLGPAQGVGF-NELIARLT 326
Qy 293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFFALGLYNGTKPLSTTSVES 352
Db 327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDMSWVSIFFALGLYNGTEGLSRTSVES 386
Qy 353 I-ETDGYAASWTVPFAARAYVENMOCAGGGGEGEKEPLVRVLVNDRVVPLHGGGVDKL 411
Db 387 AKELDGYASASWVVPFGARAYFETMCKS-----EKEPLVRALINDRVVPLHGGGVDKL 439
Qy 412 GRCKLDDFVGLSFAKSGGNWAECPA 437
Db 440 GRCKLNDFVKLSWARSGGNMGECFS 465
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Search completed: October 3, 2003, 07:47:48
Job time : 14.1257 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:51 : Search time 99.8595 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265B-27

Perfect score: 2321

Sequence: 1 NSHSGDTVDGYOCPEISHLW.....DFVEGLSFGSGNNAECFA 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2.6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2.6/ptodata/1/pubpaa/PTC_NEW_PUB.pep.*
- 3: /cgn2.6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2.6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2.6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2.6/ptodata/1/pubpaa/PTCUS_PUBCOMB.pep.*
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- 8: /cgn2.6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2.6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2.6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2.6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2.6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2.6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2.6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2.6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2.6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2.6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2.6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2020	87.0	467	14	US-10-083-452-9
2	1762.5	75.9	439	15	US-10-062-848-3
3	1762.5	75.9	449	15	US-10-062-848-12
4	1762.5	75.9	465	14	US-10-083-452-8
5	1762.5	75.9	465	15	US-10-062-848-78
6	1762.5	75.9	465	15	US-10-229-358-6
7	1762.5	75.9	474	15	US-10-213-990-24
8	1754.5	75.6	465	15	US-10-062-848-80
9	1753.5	75.5	465	15	US-10-062-848-79
10	1750.5	75.4	465	15	US-10-062-848-81
11	1707.5	73.6	469	15	US-10-062-848-82
12	1684	72.6	444	15	US-10-062-848-1
13	1684	72.6	467	15	US-10-079-709-32
14	1684	72.6	467	15	US-10-229-358-5
15	1676.5	72.2	447	15	US-10-062-848-6

16	1676.5	72.2	463	14	US-10-083-452-10
17	1672	72.0	443	9	US-09-929-060-1
18	1672	72.0	467	9	US-09-929-060-3
19	1672	72.0	467	14	US-10-083-452-11
20	1667	71.8	443	9	US-09-929-060-2
21	1660	71.5	462	15	US-10-229-358-12
22	1596.5	68.8	450	15	US-10-062-848-9
23	1596.5	68.8	466	14	US-10-083-452-13
24	1589	68.5	438	15	US-10-062-848-2
25	1588	68.4	450	15	US-10-062-848-15
26	1562.5	67.3	466	14	US-10-083-452-12
27	1562.5	67.3	466	15	US-10-229-358-7
28	1519	65.4	489	15	US-10-229-358-4
29	1519	65.4	499	15	US-10-229-358-10
30	1470	63.3	410	15	US-10-229-358-11
31	1322	57.0	475	14	US-10-083-452-14
32	1275.5	55.0	487	14	US-10-083-452-15
33	1275.5	55.0	487	15	US-10-229-358-8
34	1230.5	53.0	355	15	US-10-229-358-15
35	1185	51.1	478	14	US-10-083-452-3
36	1185	51.1	495	14	US-10-083-452-2
37	841	36.2	284	15	US-10-229-358-19
38	837.5	36.1	443	14	US-10-083-452-5
39	825	35.5	283	15	US-10-229-358-9
40	825	35.5	283	15	US-10-229-358-24
41	812.5	35.0	453	14	US-10-083-452-6
42	804.5	34.7	439	14	US-10-083-452-7
43	793	34.2	442	14	US-10-083-452-4
44	663	28.6	212	15	US-10-229-358-16
45	372.5	16.6	312	15	US-10-229-358-21

ALIGNMENTS

RESULT 1
US-10-083-452-9
Sequence 9, Application US/10083452
Publication: No. US20020127218A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Phytase Variants
FILE REFERENCE: 5618,500-US
CURRENT APPLICATION NUMBER: US/10/083.452
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: US/09/273,871
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: PA 1998 00407
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: PA 1998 00806
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: PA 1998 01176
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: PA 1999 00091
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/080,129
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/090,675
PRIOR FILING DATE: 1998-06-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 467
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 87.0%; Score 2020; DB 14; Length 467;
Best Local Similarity 89.38; Pred. No. 6.3e-197;
Matches 400; Conservative 10; Mismatches 20; Indels 18; Gaps 10;

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RESULT 8
US -0 062-848-80
: Sequence 80, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: VAN LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 80
: LENGTH: 465
: TYPE: PR
: ORGANISM: Aspergillus fumigatus

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US-10-062-848-80

Query Match 75.6%; Score 1754.5; DB 15; Length 465;
Best Local Similarity 77.1%; Pred. No. 7.2e-170;
Matches 344; Conservative 36; Mismatches 49; Indels 17; Gaps 10;

QY 2 SHSCDVTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARYP 59
DB 27 SKSCDVTDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

QY 60 TSSKSKKYSALIERIOKNAT-FKGKYAFKLTNYNTLGAADLTTPFGHQMVNSGIKFYRRY 118
DB 87 TSSKSKKYYKKLVTAIOANATDFKGKFAFLKTYNTLGAADLTTPFGEQQLVNSGIKFYQRY 146

QY 119 KALARNIVPVRASGSDRVIAAEKFIQFOSAKLADP--AHQASPVINVIIPGSGYNN 176
DB 147 KALARSVVPFIRASGSDRVIAASGEKFIQFQAKLADPGATNRAAPAIISVPIPESETFNN 206

QY 177 TLDHGLCTAFEDSTLGDAAENFTAVFAPPRIARLEA-LPGVNLTDDEVDVNLMDMCPDT 235
DB 207 TLDHGVCCTFEASQLGDEVAANFTALFADPDIRARAEKHLPGVTLTDEDVVSMDMCSFDI 266

QY 236 VARTSDATOLSPFCDLFTADEW-QYDYLSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
DB 267 VARTSDASQLSPFCQLFTHNEKKYNYLSLQSLKYYGYGAGNPLGPAQGVGF-NELIARLT 326

QY 293 HSPVQDHTSTNLTDSNPATFPLNATLYADFSHNTWVSIFFALGLYNGTGPLSTTSVES 352
DB 327 RSPVQDHTSTNLTSLVSNPATFPLNATMYVDFSHDMSVSIFFALGLYNGTGPLSTTSVES 386

QY 353 I-ETDGYAASWTVPFAARAYEMMOCEAGGGGGEKEPLVRVLVNDRVVPLHGGGVDKL 411
DB 387 AKELDYSASVWVPFCARAYFETMCKS-----EKEPLVRALINDRVVPLHGGGVDKL 439

QY 412 GRCKLDDFVEGLSFARSGGNWAECPA 437
DB 440 GRCKLNDFVKLSWARSNGNMGECFS 465

RESULT 9
US-10-062-848-79

: Sequence 79, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 79
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus

US-10-062-848-79

Query Match 75.5%; Score 1753.5; DB 15; Length 465;
Best Local Similarity 77.1%; Pred. No. 9.1e-170;
Matches 344; Conservative 36; Mismatches 49; Indels 17; Gaps 10;

QY 2 SHSCDVTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARYP 59
DB 27 SKSCDVTDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

QY 60 TSSKSKKYSALIERIOKNAT-FKGKYAFKLTNYNTLGAADLTTPFGHQMVNSGIKFYRRY 118
DB 87 TSSKSKKYYKKLVTAIOANATDFKGKFAFLKTYNTLGAADLTTPFGEQQLVNSGIKFYQRY 146

QY 119 KALARNIVPVRASGSDRVIAAEKFIQFOSAKLADP--AHQASPVINVIIPGSGYNN 176
DB 147 KALARSVVPFIRASGSDRVIAASGEKFIQFQAKLADPGATNRAAPAIISVPIPESETFNN 206

QY 177 TLDHGLCTAFEDSTLGDAAENFTAVFAPPRIARLEA-LPGVNLTDDEVDVNLMDMCPDT 235
DB 207 TLDHGVCCTFEASQLGDEVAANFTALFADPDIRARAEKHLPGVTLTDEDVVSMDMCSFDI 266

QY 236 VARTSDATOLSPFCDLFTADEW-QYDYLSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
DB 267 VARTSDASQLSPFCQLFTHNEKKYNYLSLQSLKYYGYGAGNPLGPAQGVGF-NELIARLT 326

QY 293 HSPVQDHTSTNLTDSNPATFPLNATLYADFSHNTWVSIFFALGLYNGTGPLSTTSVES 352
DB 327 RSPVQDHTSTNLTSLVSNPATFPLNATMYVDFSHDMSVSIFFALGLYNGTGPLSTTSVES 386

QY 353 I-ETDGYAASWTVPFAARAYEMMOCEAGGGGGEKEPLVRVLVNDRVVPLHGGGVDKL 411
DB 387 AKELDYSASVWVPFCARAYFETMCKS-----EKEPLVRALINDRVVPLHGGGVDKL 439

QY 412 GRCKLDDFVEGLSFARSGGNWAECPA 437
DB 440 GRCKLNDFVKLSWARSNGNMGECFS 465

RESULT 10
US-10-062-848-81

: Sequence 81, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 81
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus

US-10-062-848-81

Query Match 75.4%; Score 1750.5; DB 15; Length 465;
Best Local Similarity 76.9%; Pred. No. 1.8e-169;
Matches 343; Conservative 37; Mismatches 49; Indels 17; Gaps 10;

QY 2 SHSCDVTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARYP 59
DB 27 SKSCDVTDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

QY 60 TSSKSKKYSALIERIOKNAT-FKGKYAFKLTNYNTLGAADLTTPFGHQMVNSGIKFYRRY 118
DB 87 TSSKSKKYYKKLVTAIOANATDFKGKFAFLKTYNTLGAADLTTPFGEQQLVNSGIKFYQRY 146

QY 119 KALARNIVPVRASGSDRVIAAEKFIQFOSAKLADP--AHQASPVINVIIPGSGYNN 176
DB 147 KALARSVVPFIRASGSDRVIAASGEKFIQFQAKLADPGATNRAAPAIISVPIPESETFNN 206

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QY 236 VARTSDATOLSPCDLFTADEW-QYDIQSL-KYGYGAGNPLGPAQGVGR-NELIARLT 292
Db 267 VARTSDASQSPFCQLFTHNEWKKNYLOSGLKYGYGAGNPLGPAQGVGR-NELIARLT 326
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Db 327 RSPVQDHTSTNLTVSNPATFPLNATMYVDESHDMSWVSIFPAGLNGTKPLSTTSVES 386
QY 353 I-ETDGYAASWTVPFAARAYVENMOCEAGGGGEGEKEPLVRVLYNDRVVPPLHGGCVDKL 411
Db 387 AKELDGYASASWVPFGARAYFETMOCKS-----EKEPLVRALINDRVVPLHGGCVDKL 439
QY 412 GRCKLDDFVEGLSFARSGGNWAECEFA 437
Db 440 GRCKLNDVFKGLSWARSGGNWAECEFS 465

RESULT 11
US-10-062-848-82
: Sequence 82, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn ver. 2.1
: SEQ ID NO 82
: LENGTH: 469
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-10-062-848-82

Query Match 73.68; Score 1707.5; DB 15; Length 463;
Best Local Similarity 74.49; Pred. No. 4, 5e-165;
Matches 332; Conservative 49; Mismatches 48; Indels 17; Gaps 10;

QY 2 SHSCDTVD-GYQC-PEISHLWGYSPFFSLADESAISPDPKGCRTVFQVLSRHGARY 59
Db 31 SKACDTVELGYQCSPGTSHLWGYSPFFSLEDELVSOLDPKDCRTVFQVLSRHGARY 90
QY 60 TSSSKKYSALIERIQKNA-TPKGYAFLKTYNTLGCADDLTFFGQNMVNSGKIFERY 118
Db 91 TASKSKKKYKLVTAIQKNAFEFKGFAFLETYNTLGCADDLTFFGQNMVNSGKIFERY 150
QY 119 KALARNIVPFVRASGSDRVIAAEKFTIEGFSQAKLADP---AHOASPVINVIPEGSY 176
Db 151 KALAGSVVPFIRSSGSDRVIAAEKFTIEGFSQAKLADP---AHOASPVINVIPEGSY 210
QY 177 TLDHGLCTAFEDSTLGDAAENFTAVFAPPIARLEA-LPGVNLTDDEDVVLNMDKCPEDT 235
Db 211 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRAKKHLPGVLTDEOVVSLMDMCSFDI 270
QY 236 VARTSDATOLSPCDLFTADEW-QYDIQSL-KYGYGAGNPLGPAQGVGR-NELIARLT 292
Db 271 VARTADASELSPFCALFTHNEWKKNYLOSGLKYGYGAGNPLGPAQGVGR-NELIARLT 330
QY 293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWVSIFPAGLNGTKPLSTTSVES 352
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Db 331 NSVDQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWVSIFPAGLNGTKPLSTTSVES 390
QY 353 I-ETDGYAASWTVPFAARAYVENMOCEAGGGGEGEKEPLVRVLYNDRVVPPLHGGCVDKL 411
Db 391 TKSNGYSASWVPFGARAYFETMOCKS-----EKEPLVRALINDRVVPLHGGCVDKL 443
QY 412 GRCKLDDFVEGLSFARSGGNWAECEFA 437
Db 444 GRCKLNDVFKGLSWARSGGNWAECEFS 469

RESULT 12
US-10-062-848-81
: Sequence 1, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn ver. 2.1
: SEQ ID NO 1
: LENGTH: 444
: TYPE: PRT
: ORGANISM: Aspergillus niger
US-10-062-848-81

Query Match 72.68; Score 1684; DB 15; Length 444;
Best Local Similarity 73.98; Pred. No. 1e-162;
Matches 331; Conservative 40; Mismatches 59; Indels 18; Gaps 10;

QY 1 NSHSCDTVD-GYQC-PEISHLWGYSPFFSLADESAISPDPKGCRTVFQVLSRHGARY 58
Db 4 NOSSCDTVDOGYOCFSETSHLWGYAPFFSLANESVISPEVPAGCRVTTAQLSRUGARY 63
QY 59 PTSSKSKKYSALIERIQKNA-TPKGYAFLKTYNTLGCADDLTFFGQNMVNSGKIFERY 117
Db 64 PTDSKSKKYSALIERIQKNA-TPKGYAFLKTYNTLGCADDLTFFGQNMVNSGKIFERY 123
QY 118 YKALARNIVPFVRASGSDRVIAAEKFTIEGFSQAKLADP---AHOASPVINVIPEGSY 174
Db 124 YESLTRNIVPFIRSSGSDRVIAAEKFTIEGFSQAKLADP---AHOASPVINVIPEGSY 183
QY 175 NTLHGLCTAFEDSTLGDAAENFTAVFAPPIARLEA-LPGVNLTDDEDVVLNMDKCP 233
Db 184 NTLDPGCTVFEDELAEANFTAVFAPPIARLEA-LPGVNLTDDEDVVLNMDKCP 243
QY 234 DTVARTSDATOLSPCDLFTADEW-QYDIQSL-KYGYGAGNPLGPAQGVGR-NELIAR 290
Db 244 DTISTVDTKLSFCDLFTHDEWYDYLOSLLKYGHGAGNPLGPTQGVYANELIAR 303
QY 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWVSIFPAGLNGTKPLSTTSV 350
Db 304 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWVSIFPAGLNGTKPLSTTSV 363
QY 351 ESI-ETDGYAASWTVPFAARAYVENMOCEAGGGGEGEKEPLVRVLYNDRVVPPLHGGCV 409
Db 364 ENITQDGFSSAVTVPFAARAYVENMOCEAGGGGEGEKEPLVRVLYNDRVVPPLHGGCV 416
QY 410 KLGRCKLDDFVEGLSFARSGGNWAECEFA 437
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Db 417 ALGRCIRDSFVRGLSFARSGGDWAECEFA 444

RESULT 13

US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcum
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Sellen
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mortison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-079-709-32

Query Match 72.6%, Score 1684; DB 15; Length 467;
Best Local Similarity 73.9%; Pred. No. 1,1e-152;
Matches 331; Conservative 40; Mismatches 59; Indels 18; Gaps 10;
QY 1 NNSHCDTVD-GYQC-PEISHLWGOYSPFESLADESALSDVPKGCRTVTFVGLSRHGARY 58
DB 27 NQSCDVTVDGQYQCFSEISHLWGOYAPFFSLANESVISPEVPAGCKVTFQVLSRHGARY 86
QY 59 PTSSKSKKYSALIERIQKNA-TFKGKYAFKTYNYTLGADDLTPFGENQMVNSGKIFYRR 117
DB 87 PTDSKGGKYSALIEIOONATTFDGKYAFKTYNSILGADDLTPFGEOELVNSGKIFYOR 146
QY 118 YKALARNIVFVRASGSDRVIASAEKFIQFQSAKLADP---AHQASPVINVIPEGSY 174
DB 147 YESLTRNIVPFRSSGSSRVIASGKKFIEGQSTKLKDPRAQPGQSSPKIDVIVISEASS 206
QY 175 NNTLDHGLCTAFEDSTLGDAAEANTAVFAPPIRABLE-ALPGVNLTDDEVNLMDCPF 233
DB 207 NNTLDPGCTCFEDELADTVEANFTATFVPSIQRLNDLSGVTLTDEVTYLMDCSF 266
QY 234 DTVARTSDATOLSPFCDLFTADEW-OYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
DB 267 DTISTVDTKLSPFCDLFTDHEWINDYLOSLKYYKGAGNPLGPTQGVGYANELIAR 326
QY 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWYSIFFALGLYNGTKPLSTTSV 350
DB 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSHDNTWYSIFFALGLYNGTKPLSTTSV 386
QY 351 ESI-ETDGYAASWTVPFAARAYVEMMOCEAGGGEKEPLVRVLYNDRVPLHGCGVD 409
DB 387 ENITQDGFSSAWTVPFAARAYVEMMOCEAGGGEKEPLVRVLYNDRVPLHGCGVD 439

QY 234 DIVARTSDATOLSPFCDLFTADEW-OYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
DB 267 DTISTVDTKLSPFCDLFTDHEWINDYLOSLKYYKGAGNPLGPTQGVGYANELIAR 326
QY 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWYSIFFALGLYNGTKPLSTTSV 350
DB 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSHDNTWYSIFFALGLYNGTKPLSTTSV 386
QY 351 ESI-ETDGYAASWTVPFAARAYVEMMOCEAGGGEKEPLVRVLYNDRVPLHGCGVD 409
DB 387 ENITQDGFSSAWTVPFAARAYVEMMOCEAGGGEKEPLVRVLYNDRVPLHGCGVD 439
QY 410 KIGRCKLDDPVEGLSFARSGGDWAECEFA 437
DB 440 ALGRCIRDSFVRGLSFARSGGDWAECEFA 467
RESULT 14
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ IDS NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-229-358-5

Query Match 72.6%, Score 1684; DB 15; Length 467;
Best Local Similarity 73.9%; Pred. No. 1,1e-152;
Matches 331; Conservative 40; Mismatches 59; Indels 18; Gaps 10;
QY 1 NNSHCDTVD-GYQC-PEISHLWGOYSPFESLADESALSDVPKGCRTVTFVGLSRHGARY 58
DB 27 NQSCDVTVDGQYQCFSEISHLWGOYAPFFSLANESVISPEVPAGCKVTFQVLSRHGARY 86
QY 59 PTSSKSKKYSALIERIQKNA-TFKGKYAFKTYNYTLGADDLTPFGENQMVNSGKIFYRR 117
DB 87 PTDSKGGKYSALIEIOONATTFDGKYAFKTYNSILGADDLTPFGEOELVNSGKIFYOR 146
QY 118 YKALARNIVFVRASGSDRVIASAEKFIQFQSAKLADP---AHQASPVINVIPEGSY 174
DB 147 YESLTRNIVPFRSSGSSRVIASGKKFIEGQSTKLKDPRAQPGQSSPKIDVIVISEASS 206
QY 175 NNTLDHGLCTAFEDSTLGDAAEANTAVFAPPIRABLE-ALPGVNLTDDEVNLMDCPF 233
DB 207 NNTLDPGCTCFEDELADTVEANFTATFVPSIQRLNDLSGVTLTDEVTYLMDCSF 266
QY 234 DTVARTSDATOLSPFCDLFTADEW-OYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
DB 267 DTISTVDTKLSPFCDLFTDHEWINDYLOSLKYYKGAGNPLGPTQGVGYANELIAR 326
QY 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWYSIFFALGLYNGTKPLSTTSV 350
DB 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSHDNTWYSIFFALGLYNGTKPLSTTSV 386
QY 351 ESI-ETDGYAASWTVPFAARAYVEMMOCEAGGGEKEPLVRVLYNDRVPLHGCGVD 409
DB 387 ENITQDGFSSAWTVPFAARAYVEMMOCEAGGGEKEPLVRVLYNDRVPLHGCGVD 439

Search completed: October 3, 2003, 08:12:29
Job time : 100.859 secs

GenScore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:51 : Search time 106.714 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265B-26

Perfect score: 2470

Sequence: 1 MGFFVLLSIATLFGTSG7.....DFVEGLSFARSGGNWEEFA 457

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2311	93.6	467	14	US-10-083-452-9
2	1902	77.0	465	14	US-10-083-452-8
3	1902	77.0	465	15	US-10-062-848-78
4	1902	77.0	465	15	US-10-229-358-6
5	1895.5	76.7	474	15	US-10-213-990-24
6	1894	76.7	465	15	US-10-062-848-80
7	1893	76.6	465	15	US-10-062-848-79
8	1892.5	76.6	439	15	US-10-062-848-3
9	1892.5	76.6	449	15	US-10-062-848-12
10	1890	76.5	465	15	US-10-062-848-81
11	1868	75.6	469	15	US-10-062-848-82
12	1862	75.4	467	15	US-10-079-709-32
13	1862	75.4	467	15	US-10-229-358-5
14	1855	75.1	467	9	US-09-929-060-3
15	1850	74.9	467	14	US-10-083-452-11

Sequence 12, Appli
Sequence 1, Appli
Sequence 10, Appli
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Sequence 2, Appli
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ALIGNMENTS

RESULT 1
US-10-083-452-9
Sequence 9, Application US/10083452
Publication No. US20020127218A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Phytase Variants
FILE REFERENCE: 5618.500-US
CURRENT APPLICATION NUMBER: US/10/083.452
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: US/09/273.671
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: PA 1998 00407
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: PA 1998 00806
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: PA 1998 01176
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: PA 1999 00091
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/080,129
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/090,675
PRIOR FILING DATE: 1998-06-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 467
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 93.6% Score 2311; DB 14; Length 467;
Best Local Similarity 93.1%; Pred. No. 5.9e-225;
Matches 435; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

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Db 1 MGVEVLLSTATLFGSTGCTALGPRGNHSCDVTGGYOCFPEISHLWGQYSPFFSLEDE 60
Qy 61 SAISPDVPKCRVTFVQVLSRHGARYPTSSKKYSALIEAIOKNATAFKGYAFLKTYN 120
Db 61 SAISPDVPDCRVTFVQVLSRHGARYPTSSKKYSALIEAIOKNATAFKGYAFLKTYN 120
Qy 121 YTLGADDLTPFGQGMVNSGKIFRYRYKALARKIVPFRASGSDRVIASAEKFIEGFOSA 180
Db 121 YTLGADDLTPFGQGMVNSGKIFRYRYKALARKIVPFRASGSDRVIASAEKFIEGFOSA 180
Qy 181 KLADPGANPHQASPVNVIIPGAGYNNLTLDHGLCTAFEESELGDDVEANFTAVFAPDIR 240
Db 181 KLADPGANPHQASPVNVIIPGAGYNNLTLDHGLCTAFEESELGDDVEANFTAVFAPDIR 240
Qy 241 ARLEAHLPGVNLTDDEVNLMDCPFTVARTSDATQLSPFCDLTHDEWIOYDYLQSLG 300
Db 241 ARLEAHLPGVNLTDDEVNLMDCPFTVARTSDATQLSPFCDLTHDEWIOYDYLQSLG 300
Qy 301 KYCYGAGNPLGPAQGVGFVNELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
Db 301 KYCYGAGNPLGPAQGVGFVNELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
Qy 361 HONTMYSIFFALGLYNGTKPLSTTSVESIEETDGYAASNTVPFAARAYVEMMOCEAKEP 420
Db 361 HONTMYSIFFALGLYNGTKPLSTTSVESIEETDGYAASNTVPFAARAYVEMMOCEAKEP 420
Qy 421 LVRVLNDRVVPVPHGCGVDKLGCRKDDFVEGLSFARSGGNWEECPA 467
Db 421 LVRVLNDRVVPVPHGCGVDKLGCRKDDFVEGLSFARSGGNWEECPA 467
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RESULT 2
US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618 500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-083-452-8

Query Match 77.08; Score 1902; DB 14; Length 465;
Best Local Similarity 77.18; Pred. No. 1.5e-183;
Matches 360; Conservative 37; Mismatches 68; Indels 2; Gaps 2;

Qy 1 MGVEVLLSTATLFGSTGCTALGPRGNHSCDVTGGYOCFPEISHLWGQYSPFFSLADE 60
Db 1 MVTLTLLSAYLLSGRVSAAPSAG-SKSCDVTDLGYOCSPATSHLWGQYSPFFSLEDE 59
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Qy 61 SAISPDVPKCRVTFVQVLSRHGARYPTSSKKYSALIEAIOKNATAFKGYAFLKTYN 120
Db 60 LSVSSKLPKDCRITTLVQVLSRHGARYPTSSKKYKLVTAIOANATDFKGFALKTYN 119
Qy 121 YTLGADDLTPFGQGMVNSGKIFRYRYKALARKIVPFRASGSDRVIASAEKFIEGFOSA 180
Db 120 YTLGADDLTPFGQGMVNSGKIFRYRYKALARKIVPFRASGSDRVIASAEKFIEGFOSA 179
Qy 181 KLADPGANPHQASPVNVIIPGAGYNNLTLDHGLCTAFEESELGDDVEANFTAVFAPDIR 240
Db 180 KLADPGAT-NRAAPASVITPESETFNNTLDHGLCTAFEESELGDDVEANFTAVFAPDIR 238
Qy 241 ARLEAHLPGVNLTDDEVNLMDCPFTVARTSDATQLSPFCDLTHDEWIOYDYLQSLG 300
Db 239 ARLEKHLPGVNLTDDEVNLMDCPFTVARTSDASQLSPFCOLTHNEWKYNYLQSLG 298
Qy 301 KYCYGAGNPLGPAQGVGFVNELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
Db 299 KYCYGAGNPLGPAQGVGFVNELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 358
Qy 361 HONTMYSIFFALGLYNGTKPLSTTSVESIEETDGYAASNTVPFAARAYVEMMOCEAKEP 420
Db 359 HONMSWIFFALGLYNGTKPLSTTSVESAKELDGYSASVVPFGARAYFETMOCKSEKEP 418
Qy 421 LVRVLNDRVVPVPHGCGVDKLGCRKDDFVEGLSFARSGGNWEECPA 467
Db 419 LVRALINDRVVPLHGCVDVKGCRKLDNFVKGLSWARSGGNWEEGCF 465
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RESULT 3
US-10-062-848-78
; Sequence 78, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolp'us
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-78
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Query Match 77.08; Score 1902; DB 15; Length 465;
Best Local Similarity 77.18; Pred. No. 1.5e-183;
Matches 360; Conservative 37; Mismatches 68; Indels 2; Gaps 2;

Qy 1 MGVEVLLSTATLFGSTGCTALGPRGNHSCDVTGGYOCFPEISHLWGQYSPFFSLADE 60
Db 1 MVTLTLLSAYLLSGRVSAAPSAG-SKSCDVTDLGYOCSPATSHLWGQYSPFFSLEDE 59
Qy 61 SAISPDVPKCRVTFVQVLSRHGARYPTSSKKYSALIEAIOKNATAFKGYAFLKTYN 120
Db 60 LSVSSKLPKDCRITTLVQVLSRHGARYPTSSKKYKLVTAIOANATDFKGFALKTYN 119
Qy 121 YTLGADDLTPFGQGMVNSGKIFRYRYKALARKIVPFRASGSDRVIASAEKFIEGFOSA 180
Db 120 YTLGADDLTPFGQGMVNSGKIFRYRYKALARKIVPFRASGSDRVIASAEKFIEGFOSA 179
Qy 181 KLADPGANPHQASPVNVIIPGAGYNNLTLDHGLCTAFEESELGDDVEANFTAVFAPDIR 240
```


; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PR1
; ORGANISM: Aspergillus fumigatus
US-10-062-848-80

Query Match 76.7%; Score 1894; DB 15; Length 465;
Best Local Similarity 76.9%; Pred. No. 9.7e-183;
Matches 359; Conservative 37; Mismatches 69; Indels 2; Gaps 2;

QY 1 MGCVVLLSIATLFGSTSGTALGPRGNHSCDVGOCYCFPEISHLWGOXSPFSLADE 60
Db 1 MVTLLFLLSAAYLLSGRVSAAPSSAG-SKSCDVLGOCSPATSHLWGOXSPFSLADE 59

QY 61 SAISPDPVKGRVTFVOVLSPHGRARYPTSSKKYSALIEATOKNATAFKGYAPLKTYN 120
Db 60 LSVSKLPPKDCRITLVOLVSRHGARYPTSSKKYKLVTAIQANATDFKGFAPLKTYN 119

QY 121 YTLGADDLTPGEGQVMNSGIFKRYRYKALARKIVFVRASGSDRVIASAEKFIEGFOA 180
Db 120 YTLGADDLTPGEGQVMNSGIFKRYRYKALARSVPFIRASGSDRVIASAEKFIEGFOA 179

QY 181 KLADGANPHOASPVINVIIEGAGYNNTLDHGLCTAFESSELGDDVEANTAFAPPIR 240
Db 180 KLADPGAT-NRAAPAIISVIIPESETFNLDHGVCTKFEASOLGDEVAANTAFAPDIR 238

QY 241 ARLEAHLPGVNLTDVYVNLDMCPEDTVARTSDATQLSDFCDLFTHDFWTOYDYLSLG 300
Db 239 ARAEKHLPGVTLTDVYVNLDMCSEPTVARTSDASQLSPFCQLFTHNEWKYNYLSLG 298

QY 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
Db 299 KYGYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 358

QY 361 HDNTMVSITFFALGNGTKPLSTTSVESIEEDGYAASWTVPFAARAYVENMQCEAEKFP 420
Db 359 HDNSMVSITFFALGNGTKPLSTTSVESIEEDGYAASWTVPFAARAYVENMQCEAEKFP 418

QY 421 LVRVLNDRVYVPLHGCGVDKLGCRKRDFFVEGLSFARSGGNNEECFA 467
Db 419 LVRALINDRVYVPLHGCDVDKLGCRCKLNDFFVKGLSWARSGGNNGECFS 465

RESULT 7
US-10-062-848-79
; Sequence 79, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718

; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 465
; TYPE: PR1
; ORGANISM: Aspergillus fumigatus
US-10-062-848-79

Query Match 76.6%; Score 1893; DB 15; Length 465;
Best Local Similarity 76.9%; Pred. No. 1.2e-182;
Matches 359; Conservative 37; Mismatches 69; Indels 2; Gaps 2;

QY 1 MGCVVLLSIATLFGSTSGTALGPRGNHSCDVGOCYCFPEISHLWGOXSPFSLADE 60
Db 1 MVTLLFLLSAAYLLSGRVSAAPSSAG-SKSCDVLGOCSPATSHLWGOXSPFSLADE 59

QY 61 SAISPDPVKGRVTFVOVLSPHGRARYPTSSKKYSALIEATOKNATAFKGYAPLKTYN 120
Db 60 LSVSKLPPKDCRITLVOLVSRHGARYPTSSKKYKLVTAIQANATDFKGFAPLKTYN 119

QY 121 YTLGADDLTPGEGQVMNSGIFKRYRYKALARKIVFVRASGSDRVIASAEKFIEGFOA 180
Db 120 YTLGADDLTPGEGQVMNSGIFKRYRYKALARSVPFIRASGSDRVIASAEKFIEGFOA 179

QY 181 KLADGANPHOASPVINVIIEGAGYNNTLDHGLCTAFESSELGDDVEANTAFAPPIR 240
Db 180 KLADPGAT-NRAAPAIISVIIPESETFNLDHGVCTKFEASOLGDEVAANTAFAPDIR 238

QY 241 ARLEAHLPGVNLTDVYVNLDMCPEDTVARTSDATQLSDFCDLFTHDFWTOYDYLSLG 300
Db 239 ARAEKHLPGVTLTDVYVNLDMCSEPTVARTSDASQLSPFCQLFTHNEWKYNYLSLG 298

QY 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
Db 299 KYGYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 358

QY 361 HDNTMVSITFFALGNGTKPLSTTSVESIEEDGYAASWTVPFAARAYVENMQCEAEKFP 420
Db 359 HDNSMVSITFFALGNGTKPLSTTSVESIEEDGYAASWTVPFAARAYVENMQCEAEKFP 418

QY 421 LVRVLNDRVYVPLHGCGVDKLGCRKRDFFVEGLSFARSGGNNEECFA 467
Db 419 LVRALINDRVYVPLHGCDVDKLGCRCKLNDFFVKGLSWARSGGNNGECFS 465

RESULT 8
US-10-062-848-3
; Sequence 3, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 439
; TYPE: PR1
; ORGANISM: Aspergillus fumigatus

US-10-062-848-3

Query Match 76.6%; Score 1892.5; DB 15; Length 439;
Best Local Similarity 80.0%; Pred. No. 1.3e-182;
Matches 352; Conservative 37; Mismatches 50; Indels 2; Gaps 1;

QY 28 SHSCDVTGQYCFPEISHLMGQYSPFFSLADESAISPDVPKRCRTVFQVLSRHGARYP 87
DB 1 SKSCDVTDLGQYQCSPATSHLMGQYSPFFSLEDELSVSSKLPKDCR:TLVQVLSRHGARYP 60
QY 88 TSSSKKYSALIEAIQKNATAFKGYAFIAKTYNTLGGADLIIPFGQOQVNSGIKFYRY 147
DB 61 TSSSKKYYKKLVTAIQANATDFKGFALAKTYNTLGGADLIIPFGQOQVNSGIKFYQRY 120
QY 148 KALARKIVPVRASGSDRVIASAEKFIQEGFQSAKLADPGANPHQASPVNVIPEGAGYN 207
DB 121 KALARSVVPFIRASGSDRVIASGEKFIQEGFQSAKLADPGAI-NRAAFAISVILPESEIFN 179
QY 208 NTLQGLCTAFEESELCDDVEANFTAVFAPPIRARLEAHLPGVNLTDDEVDVNLMDMCPED 267
DB 180 NTLQGLCTAFEESELCDDVEANFTALFADPIRARAEKHLPGVNLTDDEVDVNLMDMCPED 239
QY 268 TVARTSDATQSPCCDLTFHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 327
DB 240 TVARTSDASQSPCCDLTFHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 299
QY 328 THSPVQDHTSTNHTLDSNPATFPLNATMYVDFSHDNTWVSIFPFGALGYNTEPLSRISVE 387
DB 300 TRSPVQDHTSTNHTLDSNPATFPLNATMYVDFSHDNTWVSIFPFGALGYNTEPLSRISVE 359
QY 388 SIETDGYAASWTVPFAARAYVENMOCEAEKEPLVRLVNDRVVPLHGGCDVKGCRKLD 447
DB 360 SAKELDGYASASWVVPFARAYFETMQCKSEKEPLVRALINDRVVPLHGGCDVKGCRKLD 419
QY 448 DFVEGLSFARSGGNWCECFA 467
DB 420 DFVKGLSWARSGGNWCECFS 439

RESULT 9

US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Query Match 76.6%; Score 1892.5; DB 15; Length 449;
Best Local Similarity 80.0%; Pred. No. 1.3e-182;
Matches 352; Conservative 37; Mismatches 50; Indels 1; Gaps 1;

QY 28 SHSCDVTGQYCFPEISHLMGQYSPFFSLADESAISPDVPKRCRTVFQVLSRHGARYP 87
DB 11 SKSCDVTDLGQYQCSPATSHLMGQYSPFFSLEDELSVSSKLPKDCR:ITLVQVLSRHGARYP 70

QY 88 TSSSKKYSALIEAIQKNATAFKGYAFIAKTYNTLGGADLIIPFGQOQVNSGIKFYRY 147
DB 71 TSSSKKYYKKLVTAIQANATDFKGFALAKTYNTLGGADLIIPFGQOQVNSGIKFYQRY 130
QY 148 KALARKIVPVRASGSDRVIASAEKFIQEGFQSAKLADPGANPHQASPVNVIPEGAGYN 207
DB 131 KALARSVVPFIRASGSDRVIASGEKFIQEGFQSAKLADPGAT-NRAAFAISVILPESEIFN 189
QY 208 NTLQGLCTAFEESELCDDVEANFTAVFAPPIRARLEAHLPGVNLTDDEVDVNLMDMCPED 267
DB 190 NTLQGLCTAFEESELCDDVEANFTALFADPIRARAEKHLPGVNLTDDEVDVNLMDMCPED 249
QY 268 TVARTSDATQSPCCDLTFHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 327
DB 250 TVARTSDASQSPCCDLTFHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 309
QY 328 THSPVQDHTSTNHTLDSNPATFPLNATMYVDFSHDNTWVSIFPFGALGYNTEPLSRISVE 387
DB 310 TRSPVQDHTSTNHTLDSNPATFPLNATMYVDFSHDNTWVSIFPFGALGYNTEPLSRISVE 369
QY 388 SIETDGYAASWTVPFAARAYVENMOCEAEKEPLVRLVNDRVVPLHGGCDVKGCRKLD 447
DB 370 SAKELDGYASASWVVPFARAYFETMQCKSEKEPLVRALINDRVVPLHGGCDVKGCRKLD 429
QY 448 DFVEGLSFARSGGNWCECFA 467
DB 430 DFVKGLSWARSGGNWCECFS 449

RESULT 10

US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Query Match 76.5%; Score 1890; DB 15; Length 465;
Best Local Similarity 76.7%; Pred. No. 2.5e-182;
Matches 358; Conservative 38; Mismatches 69; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTSGTALGPAGNSHSCDVTGQYCFPEISHLMGQYSPFFSLADE 6C
DB 1 MVTLTFLLSAAVLLSGRVSAAPSSAG-SKSCDVTDLGQYQCSPATSHLMGQYSPFFSLEDE 59
QY 61 SAISPDVPKRCRTVFQVLSRHGARYPTSSSKKYSALIEAIQKNATAFKGYAFIAKTYN 120
DB 60 USVSKLKPDCRITLVQVLSRHGARYPTSSSKKYYKKLVTAIQANATDFKGFALAKTYN 119
QY 121 YTLGADLIIPFGQOQVNSGIKFYRYKALARKIVPVRASGSDRVIASAEKFIQEGFQSA 180
DB 120 YTLGADLIIPFGQOQVNSGIKFYRYKALARSVVPFIRASGSDRVIASGEKFIQEGFQSA 179

Db 61 SVISPEVPAGCVRVTAQVLSRHGARYPTDSKGGKYSALIEIQNAITFDGKYAFLXIN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFVRASGRVIAASAEKFTGFSQA 180
Db 121 YSLGADDLTPFGEQELVNSGKIFRYRYESLTRNIVPFIRSSGSSRVATASGKKFTGFSQ 180
QY 181 KLADPCANPHQASPVNIIPGAGYNNI LDHGLCTAFESSEADDEANFTAVFAPPIR 240
Db 181 KLKDPRAQPGQSPKIDVVISSEASSNNTLDPGTCTVPEDESELADTVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLTDVVDVNLDMCPDFTVARTSDATQSPFCDLTFHDEWIQYDYLSLG 300
Db 241 ORLENDLSGVLTDEVTYLDMCSEFDTISTVDTKLSPFCDLTFHDEWIQYDYLSLG 300
QY 301 KYGCGAGNPLGPAQGVFNELIARLTHSPVQDHSTNHTLDSNPATFPPLNATLYADFS 360
Db 301 KYGCGAGNPLGPTGCGVYANELIARLTHSPVHDOTSSNHTLDSNPATFPPLNATLYADFS 360
QY 361 HONTWVSIFPAGLNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVENMOCEAKEP 420
Db 361 HONGIISILFALGLNGTKPLSTTVENITQDGFSSAWTVFASRLYVENMOCEAKEP 420
QY 421 LVRVLNDRVPLHSCGVDKLGRCKRCDVEGLSFARSGGNWEECEFA 467
Db 421 LVRVLNDRVPLHGPCVDALGRCTRDSFVRGLSFARSGGNWEECEFA 467

RESULT 13
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; TITLE OF INVENTION: Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes, and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-229-358-5

Query Match 75.4%; Score 1862; DB 15; Length 467;
Best Local Similarity 74.5%; Pred. No. 1.7e-179;
Matches 348; Conservative 44; Mismatches 75; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTSGIALGPRGNSHSDTVGGYQCPPEISHLWGQYSPFSLADE 60
Db 1 MGVSAYLLPLYLLSGVTSLGLAVPASRNOSTCTVDGQYCFSETSHLWGQYAPFSLANE 60
QY 61 SAISPDVPKGCVRVTAQVLSRHGARYPTSSSKKYSALIEIQNAITFDGKYAFLXIN 120
Db 61 SVISPEVPAGCVRVTAQVLSRHGARYPTDSKGGKYSALIEIQNAITFDGKYAFLXIN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFVRASGRVIAASAEKFTGFSQA 180
Db 121 YSLGADDLTPFGEQELVNSGKIFRYRYESLTRNIVPFIRSSGSSRVATASGKKFTGFSQ 180
QY 181 KLADPCANPHQASPVNIIPGAGYNNI LDHGLCTAFESSEADDEANFTAVFAPPIR 240
Db 181 KLKDPRAQPGQSPKIDVVISSEASSNNTLDPGTCTVPEDESELADTVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLTDVVDVNLDMCPDFTVARTSDATQSPFCDLTFHDEWIQYDYLSLG 300
Db 241 ORLENDLSGVLTDEVTYLDMCSEFDTISTVDTKLSPFCDLTFHDEWIQYDYLSLG 300

QY 301 KYGCGAGNPLGPAQGVFNELIARLTHSPVQDHSTNHTLDSNPATFPPLNATLYADFS 360
Db 301 KYGCGAGNPLGPTGCGVYANELIARLTHSPVHDOTSSNHTLDSNPATFPPLNATLYADFS 360
QY 361 HONTWVSIFPAGLNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVENMOCEAKEP 420
Db 361 HONGIISILFALGLNGTKPLSTTVENITQDGFSSAWTVFASRLYVENMOCEAKEP 420
QY 421 LVRVLNDRVPLHSCGVDKLGRCKRCDVEGLSFARSGGNWEECEFA 467
Db 421 LVRVLNDRVPLHGPCVDALGRCTRDSFVRGLSFARSGGNWEECEFA 467

RESULT 14
US-09-929-060-3
; Sequence 3, Application US/0992906C
; Patent No. US20030068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHINA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYASE AND GENE ENCODING SAID PHYASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-929-060-3

Query Match 75.1%; Score 1855; DB 9; Length 467;
Best Local Similarity 73.4%; Pred. No. 8.7e-179;
Matches 343; Conservative 51; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTSGIALGPRGNSHSDTVGGYQCPPEISHLWGQYSPFSLADE 60
Db 1 MGVSAYLLPLYLLSGVTSLGLAVPASRNOSTCTVDGQYCFSETSHLWGQYAPFSLANK 60
QY 61 SAISPDVPKGCVRVTAQVLSRHGARYPTSSSKKYSALIEIQNAITFDGKYAFLXIN 120
Db 61 SAISPDVPAGCVRVTAQVLSRHGARYPTDSKGGKYSALIEIQNAITFDGKYAFLXIN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFVRASGRVIAASAEKFTGFSQA 180
Db 121 YSLGADDLTPFGEQELVNSGKIFRYRYESLTRNIVPFIRSSGSSRVATASGKKFTGFSQ 180
QY 181 KLADPCANPHQASPVNIIPGAGYNNI LDHGLCTAFESSEADDEANFTAVFAPPIR 240
Db 181 KLKDPRAQPGQSPKIDVVISSEASSNNTLDPGTCTVPEDESELADTVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLTDVVDVNLDMCPDFTVARTSDATQSPFCDLTFHDEWIQYDYLSLG 300
Db 241 ORLENDLSGVLTDEVTYLDMCSEFDTISTVDTKLSPFCDLTFHDEWIQYDYLSLG 300
QY 301 KYGCGAGNPLGPAQGVFNELIARLTHSPVQDHSTNHTLDSNPATFPPLNATLYADFS 360
Db 301 KYGCGAGNPLGPTGCGVYANELIARLTHSPVHDOTSSNHTLDSNPATFPPLNATLYADFS 360
QY 361 HONTWVSIFPAGLNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVENMOCEAKEP 420
Db 361 HONGIISILFALGLNGTKPLSTTVENITQDGFSSAWTVFASRLYVENMOCEAKEP 420

Qy 421 LVRVLNDRVPLHGGVDKLGCRCKRDDVFEGLSFARSFGGNWEECEFA 467
Db 421 LVRVLNDRVPLHGGVDKLGCRCKRDDVFEGLSFARSFGGNWEECEFA 467

Search completed: October 3, 2003, 08:12:28
Job time : 108.714 secs

RESULT 15

US-10-083-452-11
; Sequence 11, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phycase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273.871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA.1998.00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA.1998.00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA.1998.01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA.1999.00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080.129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090.675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus ficuum
US-10-083-452-11

Query Match 74.9%; Score 1850; DB 14; Length 467;
Best Local Similarity 74.1%; Pred. No. 2.8e-178;
Matches 346; Conservative 44; Mismatches 77; Indels 0; Gaps 0;
Qy 1 MGVEVLLSIATLFGSTGALCPGNHSCDVTGQYQCFEISHLWQYSPHFSLADE 60
Db 1 MGVSAYLLPLYLGLSGVLAVPASRNQSSCDTVDQGYQCFSETHLWQYAPFSLANE 60
Qy 61 SAISPQVPGCRVTFQVLSRSGARYPTSSKSKYKYSALIEAIOKNAFAKGYAFLKTYN 120
Db 61 SVISPEVPAGCRVTPAQVLSRHGARYPTDSKGYKYSALIEEIQONATTFDCKYAFKTYN 120
Qy 121 YTLGADDLTFEGEQMVNSGKIFRYRYKALARKIVPFVRASGSDRVIASAEKFIEGHQA 180
Db 121 YSLGADDLTFEGEQELVNSGKIFORYESLRTNIVPFRSSGSRVIASGKKFIEGFCST 180
Qy 181 KLADPGANPHQASPVINVIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLADPRAQPCQSPKIDVISEASSNNNTLDPGCTVFDSELDATVEANFTATFVPSIR 240
Qy 241 ARLEAHLPGVNLTDDEVNLMDCPFDIVARTSDATQLSPCEDLFTHDEWIOYDLOSLG 300
Db 241 QRLNDLSGVTOTETVYLMDCSFDITSTVDTKLSPCDLFTHDEWINYDYLOSLX 300
Qy 301 KYGYGAGNPLGPAQGVGVNELIARLTHSPVODHTSINHLDGSPATFPLNATLYADFS 360
Db 301 KYGHGAGNPLGTPQGVGVNELIARLTHSPVHDDTSSNHLTSSPATFPLKSTLYADFS 360
Qy 361 HDNMTWSIFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVENMOCQEAKEP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGESSANTVFPFASRLYVENMOCQEAQAP 420
Qy 421 LVRVLNDRVPLHGGVDKLGCRCKRDDVFEGLSFARSFGGNWEECEFA 467
Db 421 LVRVLNDRVPLHGGVDKLGCRCKRDDVFEGLSFARSFGGNWEECEFA 467

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OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:45 : Search time 12.9581 Seconds
(without alignments)
1524.850 Million cell updates/sec

Title: US-09-488-265B-26

Perfect score: 2470
Sequence: 1 MGFEVLLSLATLFGSTSGT.....DFEGLSFARSGNMEECA 467

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2311	93.6	467	4	US-09-273-871A-9
2	2185	88.5	441	3	US-09-121-425-1
3	2185	88.5	441	4	US-09-634-493A-1
4	2173	88.0	467	3	US-09-121-425-2
5	2173	88.0	467	4	US-09-634-493A-2
6	1902	77.0	465	3	US-08-868-435-33
7	1902	77.0	465	4	US-08-744-231-33
8	1902	77.0	465	4	US-09-044-718-78
9	1902	77.0	465	4	US-09-636-499-6
10	1902	77.0	465	4	US-09-273-871A-8
11	1894	76.7	465	4	US-09-044-718-80
12	1893	76.6	465	4	US-09-044-718-79
13	1892.5	76.6	439	4	US-09-044-718-3
14	1892.5	76.6	449	4	US-09-044-718-12
15	1890	76.5	465	4	US-09-044-718-81
16	1868	75.6	469	4	US-09-044-718-82
17	1866	75.5	467	1	US-07-923-724-8
18	1866	75.5	467	2	US-08-609-426A-8
19	1866	75.5	467	2	US-08-374-652C-2
20	1862	75.4	467	1	US-08-151-574-32
21	1862	75.4	467	1	US-08-146-424-20
22	1862	75.4	467	1	US-08-693-709-2
23	1862	75.4	467	2	US-08-419-448-32
24	1862	75.4	467	2	US-08-819-825-3
25	1862	75.4	467	3	US-09-163-642-3
26	1862	75.4	467	4	US-09-233-510-32
27	1862	75.4	467	4	US-09-636-499-5

28 1855 75.1 467 3 US-09-155-855-3 Sequence 3, Appli
29 1855 75.1 467 4 US-09-543-744-3 Sequence 3, Appli
30 1855 75.1 467 4 US-09-929-060-3 Sequence 3, Appli
31 1850 74.9 467 4 US-09-273-871A-11 Sequence 11, Appli
32 1843 74.6 462 4 US-09-636-499-12 Sequence 12, Appli
33 1841 74.5 466 3 US-08-868-435-12 Sequence 12, Appli
34 1841 74.5 465 4 US-08-744-231-12 Sequence 12, Appli
35 1826 73.9 466 3 US-08-868-435-35 Sequence 35, Appli
36 1826 73.9 466 4 US-08-744-231-35 Sequence 35, Appli
37 1820 73.7 444 4 US-09-044-718-1 Sequence 1, Appli
38 1813.5 73.4 463 3 US-08-868-435-23 Sequence 23, Appli
39 1813.5 73.4 463 4 US-08-744-231-29 Sequence 29, Appli
40 1813.5 73.4 463 4 US-09-273-871A-10 Sequence 10, Appli
41 1813 73.4 443 3 US-09-155-855-1 Sequence 1, Appli
42 1813 73.4 443 4 US-09-543-744-1 Sequence 1, Appli
43 1813 73.4 443 4 US-09-929-060-1 Sequence 2, Appli
44 1808 73.2 443 3 US-09-155-855-2 Sequence 2, Appli
45 1808 73.2 443 4 US-09-543-744-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-273-871A-9
: Sequence 9, Application US/09273871A

: Patent No. 6514495
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618.500-US
: CURRENT APPLICATION NUMBER: US/09/273,871A
: CURRENT FILING DATE: 1999-03-22
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: PRIOR FILING DATE: 1998-06-25
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0

: SEQ ID NO 9

: LENGTH: 467

: TYPE: PRT

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: Variation

US-09-273-871A-9

Query Match 93.6%; Score 2311; DB 4; Length 467;

Best Local Similarity 93.1%; Pred. No. 3.9e+235;
Matches 435; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Cy 1 MGFEVLLSLATLFGSTSGTALSPRGNHSCDTVDGGYOCFPE:SHLWGQYSPFFSLADE 60
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Db 1 MGFEVLLSLATLFGSTSGTALSPRGNHSCDTVDGGYOCFPE:SHLWGQYSPFFSLADE 60
|||||
Qy 61 SATSPDVPKCCRTTFVQVLSRHGARYPTSSSKKYSALIEAIOKNATAFKGYAPLKTYN 120
|||||
Db 61 SATSPDVPDCCRTTFVQVLSRHGARYPTSSSKKYSALIEAIOKNATAFKGYAPLKTYN 120
|||||
Qy 121 YTLGADDLTPFGSQQVMNSGINKFYRYKALARKIVPFVRASGSDRVINASAEKFI2GFQSA 180
|||||
Db 121 YTLGADDLTPFGSQQVMNSGINKFYRYKALARKIVPFVRASGSDRVINASAEKFI2GFQSA 180
|||||
Qy 181 KLADGANPHQASPVINVIPEGAGYNNLTDLHGLCTAFEESELGDVDVANTAVPAPPIR 240
|||||

Db 181 KLADPGSQHQASPVIDVITPEGSGYNNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Qy 241 ARLEAHLPGVNLTDDEVDVNLMDMCPDFTVARTSDATOLSPEDLFTHDEWQYDYLQSLG 300
Db 241 ARLEADPGVTLTDEDVYVLMDCMCFETVARTSDATELSPFCALFTHDEWQYDYLQSLG 300
Qy 301 KYCYGAGNPLGPAOGVGFVFNELIARLTHSPYODHTSTNHTJDSNPATFPLNATLYADFS 360
Db 301 KYCYGAGNPLGPAOGVGFANELIARLTHSPYODHTSTNHTJDSNPATFPLNATLYADFS 360
Qy 361 HDNTWISIFALGLYNGIKTSTSVESIEETDGVAAASWTVPFAARAYVEMMOCEAEKEP 420
Db 361 HDNSMISIFFALGLYNGTAPLSTTSVIESIEETDGVSAASWTVPFGARAYVEMMOCEAEKEP 420
Qy 421 LVRVLVNDVRVPLRGCGVVKLGRCKRDEVEGLSFARSGGNWEECEFA 467
Db 421 LVRVLVNDVRVPLRGCAVDKLGKCKRDFVEGLSFARSGGNWAECEFA 467

RESULT 2
US-09-121-425-1
; Sequence 1, Application US/0912:425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-1

Query Match 88.5% Score 2185; DB 3; Length 441;
Best Local Similarity 92.7% Pred No 7.1e-222;
Matches 409; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 27 NSHSCDVTDDGYQCQFPEISHLWGQYSPFFSLADESAISPDVPKGCRTVQVLSRHGARY 86
Db 1 NSHSCDVTDDGYQCQFPEISHLWGQYSPFFSLEDESAISPDVPDCCRVTTFVQVLSRHGARY 60
Qy 87 PTSSKSKYSALIEAIOKNATAFKGYAFLKTYNTYTLGADDLTPFGEQOMVNSG:KEYRR 146
Db 61 PTSSKSKAYSALIEAIOKNATAFKGYAFLKTYNTYTLGADDLTPFGENQMVNSG:KEYRR 120
Qy 147 YKALARKIVPVRASGSDRVIASAEKFIQFQSAKLADPCANPHQASPVINVLPEGAGY 206
Db 121 YKALARKIVPFIKASGSDRVIASAEKFIQFQSAKLADPCQSPHQASPVIDVILPEGSGY 180
Qy 207 NNTLDHGCTAFESSELGDDVEANFTAVFAPPTRARLEADLPGVTLTDEDVYVLMDCMCP 240
Db 181 NNTLDHGCTAFEDSELGDDVEANFTALFAPARLEADLPGVTLTDEDVYVLMDCMCP 240
Qy 267 DTVARTSDATOLSPEDLFTHDEWQYDYLQSLGKYGYGAGNPLGPAOGVGFVFNELIAR 326
Db 241 ETVARTSDATELSPFCALFTHDEWQYDYLQSLGKYGYGAGNPLGPAOGVGFANELIAR 300
Qy 327 LTHSPVQDHTSTNHTJDSNPATFPLNATLYADFSHNTWYSIFFALGLYNGIKPLSTTSV 386
Db 301 LTRSPVQDHTSTNHTJDSNPATFPLNATLYADFSHNSMISIFFALGLYNGTAPLSTTSV 360
Qy 387 ESIEETDGVAAASWTVPFAARAYVEMMOCEAEKEPLVRVLVNDVRVPLHCGVDKLGRCR 446
Db 361 ESIEETDGVSAASWTVPFGARAYVEMMOCEAEKEPLVRVLVNDVRVPLHCGCAVDKLGRCR 420

Qy 447 DDFVEGLSFARSGGNWEECEFA 467
Db 421 DDFVEGLSFARSGGNWAECEFA 441

RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634,493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-634-493A-1

Query Match 88.5% Score 2185; DB 4; Length 441;
Best Local Similarity 92.7% Pred No 7.1e-222;
Matches 409; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 27 NSHSCDVTDDGYQCQFPEISHLWGQYSPFFSLADESAISPDVPKGCRTVQVLSRHGARY 86
Db 1 NSHSCDVTDDGYQCQFPEISHLWGQYSPFFSLEDESAISPDVPDCCRVTTFVQVLSRHGARY 60
Qy 87 PTSSKSKYSALIEAIOKNATAFKGYAFLKTYNTYTLGADDLTPFGEQOMVNSG:KEYRR 146
Db 61 PTSSKSKAYSALIEAIOKNATAFKGYAFLKTYNTYTLGADDLTPFGENQMVNSG:KEYRR 120
Qy 147 YKALARKIVPVRASGSDRVIASAEKFIQFQSAKLADPCANPHQASPVINVLPEGAGY 206
Db 121 YKALARKIVPFIKASGSDRVIASAEKFIQFQSAKLADPCQSPHQASPVIDVILPEGSGY 180
Qy 207 NNTLDHGCTAFESSELGDDVEANFTAVFAPPTRARLEADLPGVTLTDEDVYVLMDCMCP 240
Db 181 NNTLDHGCTAFEDSELGDDVEANFTALFAPARLEADLPGVTLTDEDVYVLMDCMCP 240
Qy 267 DTVARTSDATOLSPEDLFTHDEWQYDYLQSLGKYGYGAGNPLGPAOGVGFVFNELIAR 326
Db 241 ETVARTSDATELSPFCALFTHDEWQYDYLQSLGKYGYGAGNPLGPAOGVGFANELIAR 300
Qy 327 LTHSPVQDHTSTNHTJDSNPATFPLNATLYADFSHNTWYSIFFALGLYNGIKPLSTTSV 386
Db 301 LTRSPVQDHTSTNHTJDSNPATFPLNATLYADFSHNSMISIFFALGLYNGTAPLSTTSV 360
Qy 387 ESIEETDGVAAASWTVPFAARAYVEMMOCEAEKEPLVRVLVNDVRVPLHCGVDKLGRCR 446
Db 361 ESIEETDGVSAASWTVPFGARAYVEMMOCEAEKEPLVRVLVNDVRVPLHCGCAVDKLGRCR 420

Qy 447 DDFVEGLSFARSGGNWEECEFA 467
Db 421 DDFVEGLSFARSGGNWAECEFA 441

RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:

; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:consensus

; OTHER INFORMATION: sequence

US-09-121-425-2

Query Match 88.0%; Score 2173; DB 3; Length 467;
Best Local Similarity 85.2%; Pred. No. 1.4e-220;
Matches 415; Conservative 13; Mismatches 19; Indels 40; Gaps 2;

Qy 1 MGVFVLLSIATLFGSTSGTALGRGNHSCDVTGQYOCFPEISHLMGOYSPFSLADE 60
Db 1 MGVFVLLSIATLFGSTSGTALGRGNHSCDVTGQYOCFPEISHLMGOYSPFSLADE 60
Qy 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKKYSALIEAQKNATAFKGYAFKLYN 120
Db 61 SAISPDVPDCCRVTFFQVLSRHGARYPTSSKKAYS-----TIN 100
Qy 121 YILGADDLTPFGEQOMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIQFQSA 180
Db 101 YILGADDLTPFGEQOMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIQFQSA 160
Qy 181 KLADPGANPHQASPVIN-----VIIPEGAGYNNLTLDHGLCTAFEE 220
Db 161 KLADPGSQPHQASPVIDLIEAQKNATAFKGYAFKLYIPEGSGYNNLTLDHGTCTAFED 220
Qy 221 SELGDDVEANFTAFAPPFIRARLEAHLPGVNLTDDEVNLMDCPFDTVARTSDATQLSP 280
Db 221 SELGDDVEANFTAFAPFIRARLEADLPVLTDEVDVYLMDCPFETVARTSDATELSP 280
Qy 281 FCDLFTHDEWQYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNH 340
Db 281 FCALFTHDEWQYDYLQSLGKYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
Qy 341 TLDSNPATFPLNATLYADFSDHNSMISIFFALGLYNGTKPLSTTSVESTTEEDGYAASWT 400
Db 341 TLDSNPATFPLNATLYADFSDHNSKISIFFALGLYNGTAPLSTTSVESTTEEDGYASWT 400
Qy 401 VPFAARAYVEMMOCEAEKEPLVRVLYVNDRVVPLHGGGVOKLGRCKRDDFVEGLSFARSGG 460
Db 401 VPFGARAYVEMMOCEAEKEPLVRVLYVNDRVVPLHGGCAVDKLGCRCKRDDFVEGLSFARSGG 460
Qy 461 NWECEFA 467
Db 461 NWAECFA 467

RESULT 5

US-09-634-493A-2
; Sequence 2, Application US/05634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634.493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121.425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-634-493A-2

Query Match 88.0%; Score 2173; DB 4; Length 467;

Best Local Similarity 85.2%; Pred. No. 1.4e-220;

Matches 415; Conservative 13; Mismatches 19; Indels 40; Gaps 2;

Qy 1 MGVFVLLSIATLFGSTSGTALGRGNHSCDVTGQYOCFPEISHLMGOYSPFSLADE 60
Db 1 MGVFVLLSIATLFGSTSGTALGRGNHSCDVTGQYOCFPEISHLMGOYSPFSLADE 60
Qy 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKKYSALIEAQKNATAFKGYAFKLYN 120
Db 61 SAISPDVPDCCRVTFFQVLSRHGARYPTSSKKAYS-----TIN 100
Qy 121 YILGADDLTPFGEQOMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIQFQSA 180
Db 101 YILGADDLTPFGEQOMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIQFQSA 160
Qy 181 KLADPGANPHQASPVIN-----VIIPEGAGYNNLTLDHGLCTAFEE 220
Db 161 KLADPGSQPHQASPVIDLIEAQKNATAFKGYAFKLYIPEGSGYNNLTLDHGTCTAFED 220
Qy 221 SELGDDVEANFTAFAPPFIRARLEAHLPGVNLTDDEVNLMDCPFDTVARTSDATQLSP 280
Db 221 SELGDDVEANFTAFAPFIRARLEADLPVLTDEVDVYLMDCPFETVARTSDATELSP 280
Qy 281 FCDLFTHDEWQYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNH 340
Db 281 FCALFTHDEWQYDYLQSLGKYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
Qy 341 TLDSNPATFPLNATLYADFSDHNSMISIFFALGLYNGTKPLSTTSVESTTEEDGYAASWT 400
Db 341 TLDSNPATFPLNATLYADFSDHNSMISIFFALGLYNGTAPLSTTSVESTTEEDGYASWT 400
Qy 401 VPFAARAYVEMMOCEAEKEPLVRVLYVNDRVVPLHGGGVOKLGRCKRDDFVEGLSFARSGG 460
Db 401 VPFGARAYVEMMOCEAEKEPLVRVLYVNDRVVPLHGGCAVDKLGCRCKRDDFVEGLSFARSGG 460
Qy 461 NWECEFA 467
Db 461 NWAECFA 467

RESULT 6

US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHYLASE ACTIVITY
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25


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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/868,435
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/744,231
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Kass, Alan P
: REGISTRATION NUMBER: 32142
: REFERENCE/DOCKET NUMBER: Case Docket 9339
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201) 235-4205
: TELEFAX: (201) 235-2363
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 465 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 104
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 119
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 205
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 228
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 337
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 374
: OTHER INFORMATION: /note="potential N-glycosylation site"
:
: US-08-868-435-33
:
: Query Match
: Best Local Similarity 77.1%; Score 1902; DB 3; Length 465;
: Matches 360; Conservative 37; Mismatches 68; Indels 2; Gaps 2;
:
: QY 1 MGVFVLLSLATLFGSTGCTALGPRGNHSCDVGQCFPEISHLWQYSPFFSLADE 60
: DB 1 MVLTITLLSAAYILSGRVSAAPSAG-SKSCDVLGQCSPTAHLWQYSPFFSLEDE 59
:
: QY 61 SAISPOVPKCRVTVQVLSRHGARYPTSSKKYSALIEATQKNATAFKGYAFPLKTYN 120
: DB 60 LSVSKLPKDCRITLVQVLSRHGARYPTSSKKYKLVTAIQANAIDFKGKFAFLKTYN 119
:
: QY 121 YTLGADDLTPFGQQWNSGKIEKRYRKALARKIYPPFVRASGSDRVIASAEKFTGFGOSA 180
: DB 120 YTLGADDLTPFGQQWNSGKIEKRYRKALARKIYPPFVRASGSDRVIASAEKFTGFGOSA 179
:
: QY 181 KLADPGANPHQASPVINVIIEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPRI 240
: DB 180 KLADPGAT-NRAAPATSVIIEPESETNNTLDHGVCTKFEASQLGDEVAANTALFAPDIR 239
:
: QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPDFTVARTSDATQLSPPCDLTHDWEIYQYLSLG 300
: DB 239 ARAEKHLPGVLTDEDVSLMDMCSFTVARTSDASQLSPFCQLETHNEWKKNYVLSLG 298
:
: QY 301 KYGYGAGNPLGPAQGVGFVNELIARLTHSPQDHTSTNHTLDSNPATFPLNATLYADFS 360
: DB 299 KYGYGAGNPLGPAQGGIGFTNELIARLTRSPQDHTSTNHTLDSNPATFPLNATLYADFS 358

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: QY 361 HDNTMVSTFEALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420
: DB 359 HDNSWVSIFFALGLYNGTEPLSRTSVESAKELOGYSASWVVPFGARAYETMOCKSEREP 418
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: QY 421 LVRVLNDRVVPLHGGCGVDKLGRCRDKDFVEGLSFARSGGNWEECPA 467
: DB 419 LVRALINDRVVPLHGGCDVDKLGRCRLKDFVKGLSWARSGGNWGECPA 465
:
: RESULT 7
: US-08-744-231-33
: Sequence 33, Application US/08744231
: Patent No. 6358722
: GENERAL INFORMATION:
: APPLICANT: Van Loon, Adolphus
: TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hoffmann-La Roche Inc.
: STREET: 340 Kingsland Street
: CITY: Nutley
: STATE: New Jersey
: COUNTRY: United States of America
: Zip: 07110
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/744,231
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/424,757
: FILING DATE: 18-APR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Kass, Alan P
: REGISTRATION NUMBER: 32142
: REFERENCE/DOCKET NUMBER: Case Docket 9339
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201) 235-4205
: TELEFAX: (201) 235-2363
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 465 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 104
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 119
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 205
: OTHER INFORMATION: /note="potential N-glycosylation site"
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: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 337
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature

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QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKKYSALIEALQKNATAFKGYAFALKTYN 120
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DT 60 LSVSSKLPKDCRITLVQLVLSRHGARYPTSSKSKKYYKLVTAIQANATDFKGAFLKTYN 119
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 121 YTLGADDLTPGEQOMVNSGKIFYRKYKALARKIVPVPRASGSDRVIAAEKPIEGFQSA 180
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 120 YTLGADDLTPGEQOLVNSGKIFYRKYKALARSVPPIRASGSDRVIAECGEPIEGFOOA 179
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 181 KLADPGANPHOASPVINVIIEPGAGYNNITLDHGLCTAFEESELSGDVEANFTAVFAPPIR 240
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 180 KLADPGAT-NRAAPAIISVILPESTFTNNTLDHGVCITKFFASQUGDEVAANFTALFAPDIR 236
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 241 ARLEAHLPGVNLTDVVYVNLMDMGPFDTVARTSDATQSPFCDLTFHDEMIOQYDXLQSLG 300
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 239 ARAEKHLPGVTLTDEDVVS LMDMSFDTVARTSDAQLSPFCQLTFHNEWKYVQLQSLG 298
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 301 KYGYGAGNPLGPAOGVGFVNELIARLTHSPVQDHTSTNHTLOSINATPLNATLYADPS 360
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 299 KYGYGAGNPLGPAOGIGFTNELIARLTHSPVQDHTSTNSTLSVNPATPLNATLYADPS 358
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 361 HNTWVSIFFALGLYNGKPLSTSVESIEETDGYAASWTVPPFAARAYVEWMCCEAEKP 420
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 359 HNSWVSIFFALGLYNGTEPLSRITSVESAKELDGYASWVPPGARARAYETMOCKSEKP 418
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 421 LVRVLNDRVWPLHGGCGVDKLGCRCKRDPFVEGLSFARSGGNWEECF 467
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 419 LVRLALNDRVWPLH6CDDVDKLGCRCKLNDVFKGLSWARSGGNWGECSF 465
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-09-636-499-6
; Sequence 6, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding

```

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? FILE REFERENCE: GC586-Z
? CURRENT APPLICATION NUMBER: US/09/636.499
? CURRENT FILING DATE: 2000-08-11
? PRIOR APPLICATION NUMBER: US 60/148,960
? PRIOR FILING DATE: 1999-08-13
? NUMBER OF SEQ ID NOS: 34
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 5
? LENGTH: 465
? TYPE: PRI
? ORGANISM: Aspergillus fumigatus
? GC-09-636-499-6

Query Match 77.0%; Score 1902; DB 4; Length 465;
Best Local Similarity 77.1%; Pred. No. 5.9e-132;
Matches 360; Conservative 37; Mismatches 68; Indels 2; Gaps 2

Qy 1 MGVEVYVLLSIATLFGSTGCTALGRPGNSHSCDITVDGYQCYCFPEISHLWGCGYSPFSLADE 60
Db 1 MWTLFLLSAAVLLSGRVSAAPSAG-SKSCDITVDLGYCSPATSHLWGCGYSPFSLADE 59
Qy 61 SAISPDVFKGCRVTFVQVLSRHGARYPTSSKSKYKYSALIEAIOKNATATPKGYAFVKTYN 120
Db 60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKYKYLKLVTAIQANATDPKGFAPFLKTYN 119
Qy 121 YTLGADDLTPFGEQQVMSNGIKFYRYRYKALARKIVPVRASGSDRVIAAEKFIIEGFQSA 180
Db 120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPPIRASGSDRVIASGEKFIIEGFQQA 179
Qy 181 KLADGCANPHQASPVNIIIEGAGYNNNTLDHGLCTAFEESELGDDVENANFTAVFAPPIR 240
Db 180 KLADPGAT-NRAAPAIISVYIIESEIFNNTLDHGVTCTKFEASQLGSDVEANFTALFAPIR 238

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RESULT 12

US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.5
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 79
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-79

Query Match 76.6%; Score 1893; DB 4; Length 465;

Best Local Similarity 76.9%; Pred. No. 5.3e-191;
Matches 359; Conservative 37; Mismatches 69; Indels 2; Gaps 2;

Qy	1	MGVFLVLLSTATLFGSTGTALPGRNHSCDVTGQYQCFPEISHLWGOYSPFFSLADE	60
Db	1	MVLTFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYOCSPATSHLWGOYSPFFSLEDE	59
Qy	61	SAISPDVPGKRVTFVQVLSRHGARYPTSSKSKYSALIEAOKNATAFKGYAFKTYN	120
Db	60	LSVSSKLPKDCRITLVQLSRHGARYPTSSKSKYKLVTAIOANATDFKGFAPFKTYN	119
Qy	121	YTLGADDLTPFGQOMVNSGKIFRYKALARKIVPVRASGSDRVIASAEKFIQFOSA	180
Db	120	YTLGADDLTPFGQOLVNSGKIFRYKALARSVPVFIASGSDRVIASGEKFIQFOOA	179
Qy	181	KLADPGANPHQASPVNIIPEGAGYNNTLDHGLCTAFEESELGDDVFANFTAVFAPTR	240
Db	180	KLADPGAT-NRAAPAISSVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDTR	238
Qy	241	ARLEAHLPGVNLTDDEVNLMDCPFDIVARTSDATOLSPFCDLFTHDWIOYDYLQSLG	300
Db	239	ARAEXHLPGVTLTDEDVSLDMCSEDTVARTSDASQLSPFCOLFTHNEWKYNYIOSLG	298
Qy	301	KYGYGAGNPLGPAQGVGVNELLARLTHSPVODHTSTNHTLDSNPATFPLNATLYADEFS	360
Db	299	KYGYGAGNPLGPAQGTGFTNELIARLTRSPVODHTSTNHTLDSNPATFPLNATLYADEFS	358
Qy	361	HONTMVSIFFALGLYNGTKPLSTTSVFSIEETDGYAASWTVPFAARAYVEMMOCEAEKEF	420
Db	359	HONSMSVIFALGLYNGTEGLSRTSVESAKELDGYASVWVPGARAYFETMOCKSEKEP	418
Qy	421	LVRVLYNDRVVPVHGGVDKLGKCKRDDVFVEGLSFARSGNNECEFA 467	
Db	419	LVRALINDRVVPLHGGVDKLGKCKLNDVFVKGLSWARSGNNGECFS 465	

RESULT 13

US-09-044-718-3
; Sequence 3, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus

; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-3

Query Match 76.6%; Score 1892.5; DB 4; Length 439;

Best Local Similarity 80.0%; Pred. No. 5.4e-191;
Matches 352; Conservative 37; Mismatches 50; Indels 2; Gaps 1;

Qy	28	SHSCDVTGQYQCFPEISHLWGOYSPFFSLADEKSAISPDVPGKRVTFVQVLSRHGARYP	87
Db	1	SKSCDVTDLGYOCSPATSHLWGOYSPFFSLEDELSVSKLPKDCRITLVQVLSRHGARYP	60
Qy	88	TSSKSKYSALIEAOKNATAFKGYAFKTYNLTGADDLTPFGQOMVNSGKIFRYRY	147
Db	61	TSSKSKYKLVTAIOANATDFKGFAPFKTYNYILGADDLTPFGQOLVNSGKIFRYQY	120
Qy	148	KALARKIVPVRASGSDRVIASAEKFIQFOSAKLADPGANPHQASPVNIIPEGAGYN	207
Db	121	KALARSVPVFIASGSDRVIASGEKFIQFOQAKLADPGAT-NRAAPAISSVIIPESETFN	179
Qy	208	NTLDHGLCTAFEESELGDDVFANFTAVFAPTRARLEAHLPGVNLTDDEVNLMDCPFD	267
Db	180	NTLDHGVCTKFEASQLGDEVAANFTALFAPDIRAREKHLPGVTLTDEDVSLDMCSE	239
Qy	268	TVARTSDATOLSPFCDLFTHDWIOYDYLQSLGKYGYGAGNPLGPAQGVGVNELLARL	327
Db	240	TVARTSDASQLSPFCOLFTHNEWKYNYIOSLGKYYGYGAGNPLGPAQGTGFTNELIARL	299
Qy	328	THSPVODHTSTNHTLDSNPATFPLNATLYADESHDNTMVSIFFALGLYNGTKPLSTTSVE	387
Db	300	TRSPVODHTSTNHTLDSNPATFPLNATMYVDFSHDMSMVSIFFALGLYNGTEPLSRTSVE	359
Qy	388	SIETDGYAASWTVPFAARAYVEMMOCEAEKEPLVRVLYNDRVVPVHGGVDKLGKCKRD	447
Db	360	SAKELDGYASVWVPGARAYFETMOCKSEKEPLVRALINDRVVPLHGGVDKLGKCKLN	419
Qy	448	DFVEGLSFARSGNNECEFA 467	
Db	420	DFVKGLSWARSGNNGECFS 439	

RESULT 14

US-09-044-718-12
; Sequence 12, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:

; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus

; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT

ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Query Match 76.6%; Score 1892.5; DB 4; Length 445;
Best Local Similarity 80.0%; Pred. No. 5.6e-191;
Matches 352; Conservative 37; Mismatches 50; Indels 1; Gaps 1;
QY 28 SHSCDVGQYCFPEISHLMGOYSPFFESLADESAISPDPVPGKCRVTFVQVLSRHGARYP 87
DB 11 SKSCOTVDLGYOCSPATSHLMGOYSPFFESLEDELSVSKLPKDCRITLVQVLSRHGARYP 70
QY 88 TSKSKKYSALIEATOKNATAPKGYAFKTYNTLTGADDLTPGEQOMVNSGKIFYRY 147
DB 71 TSKSKKYSALIEATOKNATAPKGYAFKTYNTLTGADDLTPGEQOMVNSGKIFYRY 130
QY 148 KALKARKIVFVRASGSDRVIASAEKFIQFQSAKLADPGANPHOASPVINVIIPGAGYN 207
DB 131 KALKARSVWPFIRASGSDRVIASGENFIEGFQAKLADPGAT-NRAAPAIISVIIPESETFN 189
QY 208 NTLDHGLCTAFEESELGDDVEANFTAVFAPPIRLEAHLPGVNLIDEDVNLMDKCFD 267
DB 190 NTLDHGVCYKRFASQGLGDEVAANFTALFAPDIRARERKLPVTLTDEDVNSLMDKCFD 245
QY 268 TVARTSDATQSPFCDFTHDEWIOYDYLSGLKGYGYGAGNPLGPAOGVGFVNELIARL 327
DB 250 TVARTSDASQLSPFCOLFTHNEWKKYNTYLSGLKGYGYGAGNPLGPAOGIGFTNELIARL 309
QY 328 THSPVODHTSTNHTLDSNPATPLNATLYADFSHDNTWVSIFPAGLYNGTKPLSTTSVE 367
DB 310 TRSPVODHTSTNHTLDSNPATPLNATLYADFSHDNTWVSIFPAGLYNGTEPUSRTSVE 363
QY 388 SIEETDGYAASWTVFAARAYVEMMQCEAEKEPLVRVLNDRVPLHCGGVKLGCRCKRD 447
DB 370 SAKELDGYASASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHCGDVKLGCRCKLN 429
QY 448 DFVEGLSFARSGNWECEFA 467
DB 430 DFVKGLSWARSGNMGCEFS 449

RESULT 15
US-09-044-718-81
Sequence 81, Application US/09044718
Patent No. 6391605
GENERAL INFORMATION:
APPLICANT: KOSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: van LOON, Adolphus
APPLICANT: VOGEL, Kurt
APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 81
LENGTH: 465
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-09-044-718-81

Query Match 76.5%; Score 1890; DB 4; Length 465;
Best Local Similarity 76.7%; Pred. No. 1.1e-190;
Matches 358; Conservative 38; Mismatches 69; Indels 2; Gaps 2;
QY 1 MGFEVLLSLATFGSTGALPGRNHSCDVGQYCFPEISHLMGOYSPFFESLADE 60
DB 1 MWTLITLLSAAVLLSGEVSNAPSSAG-SKSCOTVDLGYOCSPATSHLMGOYSPFFESLEDE 59

QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKKYSALIEATOKNATAPKGYAFKTYN 120
DB 60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYSALIEATOKNATAPKGYAFKTYN 119
QY 121 YTLGADDLTPGEQOMVNSGKIFYRYKALKARKIVFVRASGSDRVIASAEKFIQFQSA 180
DB 120 YTLGADDLTPGEQOMVNSGKIFYRYKALKARSVWPFIRASGSDRVIASAEKFIQFQSA 179
QY 181 KLADPGANPHOASPVINVIIPGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
DB 180 KLADPGAT-NRAAPAIISVIIPESETFNNTLDHGLCTAFEESELGDDVEANFTAVFAPDIR 238
QY 241 ARLEAHLPGVNLIDEDVNLMDKCFDPTVARTSDATQSPFCDFTHDEWIOYDYLSGL 300
DB 239 ARAKKHLPGVTLTDEDVNSLMDKCFDPTVARTSDASQLSPFCOLFTHNEWKKYNTYLSGL 298
QY 301 KYGYGAGNPLGPAOGVGFVNELIARLTHSPVODHTSTNHTLDSNPATPLNATLYADFS 360
DB 299 KYGYGAGNPLGPAOGIGFTNELIARLTHSPVODHTSTNHTLDSNPATPLNATLYADFS 358
QY 361 HDNTWVSIFPAGLYNGTKPLSTTSVESIEETDGYAASWTVFAARAYVEMMQCEAEKEP 420
DB 359 HDNSHVSIFPAGLYNGTEPUSRTSVESEKELDGYASASWVVPFGARAYFETMQCKSEKEP 418
QY 421 LVRVLNDRVPLHCGGVKLGCRCKRDDVEGLSFARSGNWECEFA 467
DB 419 LVRALINDRVVPLHCGDVKLGCRCKLNDVFKGLSWARSGNMGCEFS 465

Search completed: October 3, 2003, 07:47:46
Job time : 14.9581 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 07:48:21 : Search time 21.3866 seconds
(without alignments)
5642.336 Million cell updates/sec

Title: US-09-488-265B-25

Perfect score: 2525
Sequence: 1 tatatgaattcattgagcgtg.....ttcgttaagaattcatata 1426

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310856 residues
Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Command line parameters:

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-DB-Issued_Patents_AA -OPMT-fastan -SUFFIX=oct3.ra1 -MINMATCH=0.1 -LOC=PCCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.ccd1
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09488265 -CGCN 1.1.99 -runat_03102003_074813_12239 -NCPUS=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEC_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=180 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -FGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2311	91.5	467	4	US-09-273-871A-9	Sequence 9, Appli
2	2185	86.5	441	3	US-09-121-425-1	Sequence 1, Appli
3	2185	86.5	441	4	US-09-634-493A-1	Sequence 1, Appli
4	2173	86.1	467	3	US-09-121-425-2	Sequence 2, Appli
5	2173	86.1	467	4	US-09-634-493A-2	Sequence 2, Appli
6	1902	75.3	465	3	US-08-868-435-33	Sequence 33, Appl
7	1902	75.3	465	4	US-08-744-231-33	Sequence 33, Appl
8	1902	75.3	465	4	US-09-044-718-78	Sequence 78, Appl
9	1902	75.3	465	4	US-09-636-499-6	Sequence 6, Appli
10	1902	75.3	465	4	US-09-273-871A-8	Sequence 8, Appli
11	1894	75.0	465	4	US-09-044-718-80	Sequence 80, Appl
12	1893	75.0	465	4	US-09-044-718-79	Sequence 79, Appl

13	1892.5	75.0	439	4	US-09-044-718-3	Sequence 3, Appli
14	1892.5	75.0	449	4	US-09-044-718-12	Sequence 12, Appl
15	1890	74.9	465	4	US-09-044-718-81	Sequence 81, Appl
16	1868	74.0	469	4	US-09-044-718-82	Sequence 82, Appl
17	1866	73.9	467	1	US-07-923-724-8	Sequence 8, Appli
18	1866	73.9	467	2	US-08-609-426A-8	Sequence 8, Appli
19	1866	73.9	467	2	US-08-374-652C-2	Sequence 2, Appli
20	1862	73.7	467	1	US-08-151-574-32	Sequence 20, Appl
21	1862	73.7	467	1	US-08-146-424-20	Sequence 20, Appl
22	1862	73.7	467	1	US-08-593-709-2	Sequence 2, Appli
23	1862	73.7	467	1	US-08-419-448-32	Sequence 32, Appl
24	1862	73.7	467	2	US-08-819-825-3	Sequence 3, Appli
25	1862	73.7	467	3	US-09-163-642-3	Sequence 3, Appli
26	1862	73.7	467	4	US-09-233-510-32	Sequence 32, Appl
27	1862	73.7	467	4	US-09-636-499-5	Sequence 3, Appli
28	1855	73.5	467	3	US-09-155-855-3	Sequence 3, Appli
29	1855	73.5	467	4	US-09-543-744-3	Sequence 3, Appli
30	1855	73.5	467	4	US-09-929-060-3	Sequence 3, Appli
31	1850	73.3	467	4	US-09-273-871A-11	Sequence 11, Appl
32	1843	73.0	462	4	US-09-636-499-12	Sequence 12, Appl
33	1841	72.9	466	3	US-08-868-435-12	Sequence 12, Appl
34	1841	72.9	466	3	US-08-744-231-12	Sequence 35, Appl
35	1826	72.3	466	3	US-08-868-435-35	Sequence 35, Appl
36	1826	72.3	466	4	US-08-744-231-35	Sequence 35, Appl
37	1820	72.1	444	4	US-09-044-718-1	Sequence 1, Appli
38	1813.5	71.8	463	3	US-08-868-435-29	Sequence 29, Appl
39	1813.5	71.8	463	4	US-08-744-231-29	Sequence 29, Appl
40	1813.5	71.8	443	3	US-09-155-855-1	Sequence 1, Appli
41	1813	71.8	443	4	US-09-543-744-1	Sequence 1, Appli
42	1813	71.8	443	4	US-09-929-060-1	Sequence 1, Appli
43	1813	71.8	443	3	US-09-155-855-2	Sequence 2, Appli
44	1808	71.6	443	4	US-09-543-744-2	Sequence 2, Appli
45	1808	71.6	443	4	US-09-543-744-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-273-871A-9

Sequence 9, Application US/09273871A

Patent No. 6514495

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Phytase Variants
FILE REFERENCE: 5618.500-US
CURRENT APPLICATION NUMBER: US/09/273.871A
CURRENT FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: PA 1998 00407
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: PA 1998 00806
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: PA 1998 01176
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: PA 1999 00091
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/080.129
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/090.675
PRIOR FILING DATE: 1998-06-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 467

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Variation

US-09-273-871A-9

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

6.13e-212
2311.00
95.93%

Length:
Matches:
Conservative: 13

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Db	61	ProThrSerSerLysSerLysAlaIyrSerAlaLeuIleGluAlaIleGlnLysAsnAla	80	Db	421	AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsn:trpAlaGluCysPhe	440
QY	330	ACTGCTTTCAGGGTAACTAGCTAGCTTTCTTGAAGACTTACAACTACACTTTGGTGCTGAC	389	QY	1410	GCT 1412	
Db	81	ThrAlaPheLysGlyLysAlaPheLeuLys:hrTyrAsnTyrThrLeuGlyA:aaSp	100	Db	441	Ala 441	
QY	390	GACTTGCTCCATTCGGTGAACAAAGTGAAGTCTGCTTAACTCTTAACTTCTACAGAAGA	449	RESULT 3			
Db	101	AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyLysPheTyrArgArg	120	JS-09-634-493A-1			
QY	450	TACAGGCTTTGGCTAGAAAGATTGCTCCATTGCTTASAGCTTCGTTGCTGACAGATT	509	: Sequence 1, Application US/09634493A			
Db	121	TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal	140	: Patent No. 6579975			
QY	510	ATTGCTTCTGCTGAAGCTTCATTGAAGGTTTCCAACTCGCTAAGTTGGCTACCCAGGT	569	: GENERAL INFORMATION:			
Db	141	IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProG-y	160	: APPLICANT: Lehmann, Martin			
QY	570	GCTAACCCACACCAAGCTTCTCCAGTTATTAAAGTTATTATCCAGAAGTGGCTGTTAC	629	: TITLE OF INVENTION: Consensus Phytases			
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QY	630	RACACACTTTGGACACCGGTTTGTGCTACTGCTTCCAGAAATCTGAATGGCTGACGAC	699	: CURRENT APPLICATION NUMBER: US/09/634.493A			
Db	181	AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp	750	: PRIOR FILING DATE: 2000-08-08			
QY	690	STTGAAAGTAACTTCACTGCTGTTTGGCTCCACTATTAGAGTACAGTGAAGCTCAC	749	: PRIOR APPLICATION NUMBER: US/09/121,425			
Db	201	ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp	720	: PRIOR FILING DATE: 1998-07-23			
QY	750	TGGCAGGTGTAACTGACTGACGACAGACGTTGTTAACTGTAIGGACATGTTGCTGATTC	809	: PRIOR FILING DATE: 1997-07-24			
Db	221	LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe	840	: NUMBER OF SEQ ID NOS: 20			
QY	810	GACACTGTGTAGAACTTCTGACGCTACTCAATTTGCTCCATTCTGTGACTTGTCACT	869	: SOFTWARE: PatentIn Ver. 2.0			
Db	241	GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr	260	: SEQ ID NO 1			
QY	870	CACGACGAATGGATTCAATACGACTACTTGCATCTTGGTGAAGTACTACGGTACGGT	929	: LENGTH: 441			
Db	261	HisAspGluThrProGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly	280	: TYPE: PRT			
QY	930	GCTGTAAACCACTGGGTCACGCTCAAGGCTTGGTTTGGTTAACTGTAAGTACTACGGT	989	: ORGANISM: Artificial Sequence			
Db	281	AlaGlyAsnProLeuGlyProAlaGluGlyValGlyPheAlaAsnGluLeuIleAlaArg	300	: FEATURE:			
QY	990	TGACTCACTCTCCAGTTCAAGACACACACTTCTACTAACCCACTTTGGACTCTAACCCA	1049	: OTHER INFORMATION: Description of Artificial Sequence:consensus			
Db	301	LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAspPro	320	: OTHER INFORMATION: sequence			
QY	1050	GCTACTTTCCCATTCAGCGCTACTTGTAGCTGACTTCTCTCAGCACACACTATGGTT	1109	US-09-634-493A-1			
Db	321	AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspSerMetIle	340	Alignment Scores:			
QY	1110	TCTATTCTTCTCGCTTTGGGTTTGTACACGCTACTAAGCATTTGCTACTACTTGTGT	1169	Pred. No.: 6,27e-200			
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QY	1170	GAATCTATTGAAGAACTGACGGTTACGCTGCTTCTTGGACTGTTCCATTGCTGCTAGA	1229	Percent Similarity: 95.69%			
Db	361	GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg	380	Best Local Similarity: 92.74%			
QY	1230	GCTTACGTTGAATGATCAATGTGAAGCTCAAAAGCAACCATTTGGTTTGGTTTGGTT	1289	Query Match: 86.53%			
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				Db 1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGluIleSerHis			
				QY 150 TTGCGGCTCAACTCTCCATCTCTCTTTGGCTGACGAATCTGCTATTCTCCAGAC			
				Db 21 LeuTrpGlyGlnTyrSerProTyr:PheSerLeuGluAspGluSerAlaIleSerProAsp			
				QY 210 GTTCCAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCTAGACACGGTGTAGATAC			
				Db 41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr			
				QY 270 CCAACTTCTTAAGTCTAAGAACTACTCTGCTTTGATTTGAAGTATTCAAAAGACGGT			
				Db 61 ProThrSerSerLysSerLysAlaIyrSerAlaLeuIleGluAlaIleGlnLysAsnAla			
				QY 330 ACTGCTTTCAGGGTAACTAGCTAGCTTTCTTGAAGACTTACAACTACACTTTGGTGCTGAC			
				Db 81 ThrAlaPheLysGlyLysAlaPheLeuLys:hrTyrAsnTyrThrLeuGlyAlaAsp			
				QY 390 GACTTGCTCCATTCGGTGAACAAAGTGAAGTCTGCTTAACTCTTAACTTCTACAGAAGA			
				Db 101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyLysPheTyrArgArg			
				QY 450 TACAGGCTTTGGCTAGAAAGATTGCTCCATTGCTTASAGCTTCGTTGCTGACAGATT			
				Db 121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal			
				QY 510 ATTGCTTCTGCTGAAGCTTCATTGAAGGTTTCCAACTCGCTAAGTTGGCTACCCAGGT			


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Db 141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160
QY 570 GCTAACCCACCAAGCTCTCCAGTTATTAAGCTATATATATCCAGAAGGTCCTGCTTAC 629
Db 161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr 180
QY 630 AACACACTTTGGACCAACGGTTTGTACTGCTTTGGAAGAATCTGAATTTGGGTGACGAC 689
Db 181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200
QY 690 GTTGAAGCTAACTCACTGCTTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCAC 749
Db 201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220
QY 750 TTGCAGGTGTTAACTTGACTGACGAAGAGCTGTGTTAACTTGATGCAIATGTCATTC 809
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QY 810 GACACTGTTGCTAGAACTTCTGACGCTACTCAATGCTCTCCATTCTGTGACTTGTACT 869
Db 241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260
QY 870 CACGACGAATCGGATCAATACGACTACTTGCATCTTTGGGTAAAGTACTACGTTACGGT 929
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QY 1170 GAATCTATTGAAGAACTGACGGTTACGCTGCTTCTTGACTGCTTCCATTCGCTCTAGA 1229
Db 361 GluSerIleGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380
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QY 1350 GACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATCTTC 1409
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QY 1410 GCT 1412
Db 441 Ala 441

RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus Phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
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; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-09-121-425-2
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Alignment Scores: 9,07e-199 Length: 467
Pred. No.: 2173,00 Matches: 415
Score: 87,89% Conservative: 13
Best Local Similarity: 85,22% Mismatches: 19
Query Match: 86,06% Indels: 40
DB: 3 Gaps: 2
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US-09-488-265b-25 (1-1426) x US-09-121-425-2 (1-467)

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Qy 972 AAGCAATTGATGCTAGATTGACTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 1031
Db 321 AsnGluLeuLeuAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340
Qy 1032 ACTTTGAGCTCTAACCCAGCTACTTTCCCATTTGAACGGTACTTTTGTACGCTGACTTCTCT 1031
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Db 441 LeuGlyArgCysLysArgAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
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RESULT 6
US-08-868-435-33
Sequence 33, Application US/08868435
Patent No. 6291221
GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/744,231
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc_feature
LOCATION: 104
OTHER INFORMATION: /note="potential N-glycosylation site"
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LOCATION: 337
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-868-435-33
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Score: 1902.00 Matches: 360
Percent Similarity: 85.01% Conservative: 37
Best Local Similarity: 77.09% Mismatches: 68
Query Match: 75.33% Indels: 2
DB: 3 Caps: 2
US-09-488-265B-25 (1-1426) x US-08-868-435-33 (1-465)

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Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
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Qy 312 GCTATTCAAAGNACGCTACTCTTTCAGGGTAACTAGCTTCTTCAAGACTTACAAC 371
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Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIle 198
QY 612 CCAGAAGTCTGCTGGTTTACAAACACTTTGGACCAGGTTTGTGTACTGCTTTCGAAGA 671
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Db 319 AsnGlnLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSortrAsnSer 338
QY 1032 ACTTTGGACTCTAACCCAGCTACTTCCCATTTGAACGCTACTTTGTAGCGTGACTTCTCT 1091
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
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RESULT 7
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,231
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc_feature
LOCATION: 104
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OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"

Alignment Scores:
Prod. No.: 6 6e-173 Length: 465
Score: 1902.00 Matches: 360
Percent Similarity: 85.01% Conservative: 37
Best Local Similarity: 77.09% Mismatches: 68
Query Match: 75.33% Indels: 2
Db: 4 Gaps: 2

US-09-488-265B-25 (1-1426) x US-08-744-231-33 (1-465)
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Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
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Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyGlnCys 39
QY 132 TTCCAGAAATTTCTCACTGTGGGGTCAATACCTCCATCTCTCTCTGTTGGTGGAGAA 192
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QY 40 SerProAlaThrSerHisLeuTrpGlyGlnTrpSerProPheSerLeuGluAspGlu 59
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTrpSerProPheSerLeuGluAspGlu 59
QY 192 TCTGCTATTCTCCAGAGCTTCCAAAGGGTGTAGAGTTACTTTCCTGTTCAAGTTTGTCT 251
Db 192 TCTGCTATTCTCCAGAGCTTCCAAAGGGTGTAGAGTTACTTTCCTGTTCAAGTTTGTCT 251
QY 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACACGGTGTAGATACCACTCTCTTCAAGTCTAAGAGTACTCTGCTTCAATGAA 311
Db 252 AGACACGGTGTAGATACCACTCTCTTCAAGTCTAAGAGTACTCTGCTTCAATGAA 311
QY 80 ArgHisGlyAlaArgTyProThrSerSerLysSerLysTyLysLysLeuValThr 99
Db 80 ArgHisGlyAlaArgTyProThrSerSerLysSerLysTyLysLysLeuValThr 99
QY 312 GCTATTCAAAGAAGCGTACTGCTTCAAGGGTAAAGTACGCTTCTTGAAGACTTACAAC 371
Db 312 GCTATTCAAAGAAGCGTACTGCTTCAAGGGTAAAGTACGCTTCTTGAAGACTTACAAC 371
QY 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyAsn 119
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyAsn 119
QY 372 TACACTTTGGGTGCTGACGACTTGACTCCATTCCTGCTGAGTGAACCAAAATGGTTACTCTGGT 431
Db 372 TACACTTTGGGTGCTGACGACTTGACTCCATTCCTGCTGAGTGAACCAAAATGGTTACTCTGGT 431
QY 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 432 ATTAAGTTCTACAGAAGTACAAAGGCTTTGGCTAGAAGATTTGCTTCCATTCGTTAGAGCT 491
Db 432 ATTAAGTTCTACAGAAGTACAAAGGCTTTGGCTAGAAGATTTGCTTCCATTCGTTAGAGCT 491
QY 140 IleLysPheTyGlnArgTyLysAlaLeuAlaArgSerValValProPheIleArgAla 159
Db 140 IleLysPheTyGlnArgTyLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 492 TCTGCTCTGACAGAGTTATTCCTCTCTGCTGAAAGTTCATTTGAAGTTTCCAAATCTGCT 551
Db 492 TCTGCTCTGACAGAGTTATTCCTCTCTGCTGAAAGTTCATTTGAAGTTTCCAAATCTGCT 551
QY 160 SerGlySerAspArgValIleAlaSerGlyLysPheIleGluGlyPheGlnGlnAla 179
Db 160 SerGlySerAspArgValIleAlaSerGlyLysPheIleGluGlyPheGlnGlnAla 179
QY 552 AAGTTGGTGTACCCAGGTGCTAACCCACCAACGCTTCTCCAGTTATTAAAGTTATTATT 611
Db 552 AAGTTGGTGTACCCAGGTGCTAACCCACCAACGCTTCTCCAGTTATTAAAGTTATTATT 611
QY 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 196
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 196
QY 612 CCAGAAGGTGCTGTACAAACACACTTTGACACAGGTTTGTGCTACTGCTTTCGAGAA 671
Db 612 CCAGAAGGTGCTGTACAAACACACTTTGACACAGGTTTGTGCTACTGCTTTCGAGAA 671
QY 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 672 TCTGAATGGGTGACGAGCTGAAGCTTAACCTCACTGCTGTTTTCGCTCCACCTATTAGA 731
Db 672 TCTGAATGGGTGACGAGCTGAAGCTTAACCTCACTGCTGTTTTCGCTCCACCTATTAGA 731
QY 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 236
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 236
QY 732 GCTAGATTGGAAGCTCACTTGCACGTTTAACTTGACTGACGAAGAGCTTGTAACTTG 791
Db 732 GCTAGATTGGAAGCTCACTTGCACGTTTAACTTGACTGACGAAGAGCTTGTAACTTG 791
QY 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 792 ATGGCATGTGCTCCATTCGACACTGCTGCTAGAACTTCTGACGCTACTCAATTCCTCCA 851
Db 792 ATGGCATGTGCTCCATTCGACACTGCTGCTAGAACTTCTGACGCTACTCAATTCCTCCA 851
QY 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 852 TTCTGTGACTTGTCTCACTACACAGCAATGGATTCAATACGACTACTGCAATCTTGGGT 911
Db 852 TTCTGTGACTTGTCTCACTACACAGCAATGGATTCAATACGACTACTGCAATCTTGGGT 911
QY 279 PheCysGlnLeuPheThrHisAsnGluTrpLysTyLysTyLysAsnTyLysLeuGlnSerLeuGly 298
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysTyLysTyLysAsnTyLysLeuGlnSerLeuGly 298
QY 912 AAGTACTACGGTTACGGTCTCGTAAACCATTTGGGTCCAGCTCAAGGTGTGGTTCGCT 571
Db 912 AAGTACTACGGTTACGGTCTCGTAAACCATTTGGGTCCAGCTCAAGGTGTGGTTCGCT 571
QY 299 LysTyTyGlyTyGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 316
Db 299 LysTyTyGlyTyGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 316
QY 972 AACGAATTGATTGCTAGATTGACTCTCCAGTTCAGAGTTCAGACCACTTCTACTAAACAC 1031
Db 972 AACGAATTGATTGCTAGATTGACTCTCCAGTTCAGAGTTCAGACCACTTCTACTAAACAC 1031
QY 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1032 ACTTGGACTCTAACCCAGCTACTTCCCATTTGAAGAGTACTTGTGACGCTGACTTCTCT 1091
Db 1032 ACTTGGACTCTAACCCAGCTACTTCCCATTTGAAGAGTACTTGTGACGCTGACTTCTCT 1091
QY 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyValAspPheSer 358
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyValAspPheSer 358
QY 1092 CAGCAACACTATGTTCTATTCTTCTGCTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1151
Db 1092 CAGCAACACTATGTTCTATTCTTCTGCTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTT 1151
QY 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyAsnGlyThrGluPro 378
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyAsnGlyThrGluPro 378
QY 1152 TTGCTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGGTCTGCTTCTGCACT 1211
Db 1152 TTGCTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGGTCTGCTTCTGCACT 1211
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QY 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY 1212 GTTCCATTCCGCTAGACCTTACGTTGAATGATGCAATGTGAAGCTGAAAGGACCA 1271
Db 1212 GTTCCATTCCGCTAGACCTTACGTTGAATGATGCAATGTGAAGCTGAAAGGACCA 1271
QY 399 ValProPheGlyAlaArgAlaTyPheGluThrMetGlnCysLysSerGluLysGluPro 418
Db 399 ValProPheGlyAlaArgAlaTyPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1272 TTGGTTAGAGTTTGGTTTACGACAGAGTGTTCCTATTCGACGGTGTGGGTGACAA 1331
Db 1272 TTGGTTAGAGTTTGGTTTACGACAGAGTGTTCCTATTCGACGGTGTGGGTGACAA 1331
QY 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1332 TTGGTGTAGATGTAGACAGAGACTTCTGTTCAAGTGTGTTTTCGCTAGATCTGGT 1391
Db 1332 TTGGTGTAGATGTAGACAGAGACTTCTGTTCAAGTGTGTTTTCGCTAGATCTGGT 1391
QY 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY 1392 AACTGGGAAGAAATGTTTCGCT 1412
Db 1392 AACTGGGAAGAAATGTTTCGCT 1412
QY 459 AsnTrpGlyGluCysPheSer 465
Db 459 AsnTrpGlyGluCysPheSer 465
RESULT 8
US-09-044-718-78
: Sequence 78, Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTRENA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Mark
: APPLICANT: WYSS, Kurt
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: Patent Ver. 2.1
: SEQ ID NO 78
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-09-044-718-78
Alignment Scores:
Pred. No.: 6,6e-173 Length: 465
Score: 1902.00 Matches: 360
Percent Similarity: 85.01% Conservative: 37
Best Local Similarity: 77.09% Mismatches: 68
Query Match: 75.33% Indels: 2
DB: 4 Gaps: 2
US-09-488-265b-25 (1-1426) x US-09-044-718-78 (1-465)
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Db 12 ATGGCGCTGTTTCGCTGCTACTGTCCATTCGACCTTGTTCGGTTCACATCCGGTACC 71
QY 72 GCCTTGGGCTCGTGGTGAATCTCACTCTCTGACACTGTTGACGCTGGTTACCAAGT 131
Db 72 GCCTTGGGCTCGTGGTGAATCTCACTCTCTGACACTGTTGACGCTGGTTACCAAGT 131
QY 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyGlnCys 39
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyGlnCys 39
QY 132 TTCCAGAAATTTCTCACTGTGGGGTCAATACCTCCATCTCTCTCTGTTGGTGGAGAA 191
Db 132 TTCCAGAAATTTCTCACTGTGGGGTCAATACCTCCATCTCTCTCTGTTGGTGGAGAA 191
QY 40 SerProAlaThrSerHisLeuTrpGlyGlnTrpSerProPheSerLeuGluAspGlu 59
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTrpSerProPheSerLeuGluAspGlu 59
QY 192 TCTGCTATTCTCCAGAGCTTCCAAAGGGTGTAGAGTTACTTTCCTGTTCAAGTTTGTCT 251
Db 192 TCTGCTATTCTCCAGAGCTTCCAAAGGGTGTAGAGTTACTTTCCTGTTCAAGTTTGTCT 251
QY 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACACGGTGTAGATACCACTCTCTTCAAGTCTAAGAGTACTCTGCTTCAATGAA 311
Db 252 AGACACGGTGTAGATACCACTCTCTTCAAGTCTAAGAGTACTCTGCTTCAATGAA 311
QY 80 ArgHisGlyAlaArgTyProThrSerSerLysSerLysTyLysLysLeuValThr 99
Db 80 ArgHisGlyAlaArgTyProThrSerSerLysSerLysTyLysLysLeuValThr 99
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QY 312 GCTATTCAAAGACCTACTGCTTTCAGAGGTAAAGTACGCTTCTTGAAGACTTACAAAC 371
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QY 372 TACACTTGGTGCTGACGACTGACTCCATTGGTGAACAACAATGGTTAACTCTGCT 431
DB 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 432 ATTAAGTTCTACAGAAGAACAAGGTTTGGCTAGAAAGATTGTTCCATTCTGTTAGACT 491
DB 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 492 TCTGGTCTGACAGAGTTATTGCTTCGCTGAAAGAGTTCATTGAAGGTTTCCAATCTGCT 551
DB 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179
QY 552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCGCCAGTTATTAAAGTTATTAT 611
DB 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 612 CCAGAGGTGCTGGTTACACACACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 571
DB 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 216
QY 672 TCTGAATTGGTGACGACCTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATACGA 731
DB 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProaspIleArg 236
QY 732 GTAGATTGGAGCTCACTTGGCAGGTGTTAACTTCACTGACGACGAGAGCTTGTAACTTG 751
DB 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 792 ATGGACATGTGCTCCATTCCACACTGTTGCTGACAGCTTCTGACGCTACTCAATTGCTCCA 851
DB 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 852 TCTGTGACTTGTTCACCTCAGCAGAACTGGATTCAATAGCACTACTTGCATCTTGTGGT 911
DB 279 PheCysGlnLeuPheThrHisAsnGluTrpLysTyrAsnTyrLeuGlnSerLeuGly 296
QY 912 AGTACTAGCGTTACGGTCTGTTAACCCATTGGGTCCAGCTCAAGGTGTGGTTCGTT 971
DB 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 972 AACGAATTGATTGCTAGATTGACTCCTCTCCAGTTCAGACACCACTTCTACTAACCA 1031
DB 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1032 ACTTTGGACTCTAACCCAGCTACTTCCCATTTGAACGGTACTTTGTACGCTACTCTCT 1091
DB 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1092 CAGGACAACACTATGTTCTATTCTTCTTGGGTTTGTACACGGTACTTAAGCCA 1151
DB 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAspGlyThrGluPro 376
QY 1152 TTCTCTACTACTTCTGTTCAATCTATGAAGAACTGACGGTTACGCTGCTTCTTGGACT 1211
DB 379 LeuSerArgThrSerValGluSerAlaTyrGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY 1212 GTTCCATTGCTGCTAGAGCTTACGTTGAATGATGCAATGTGAAGCTTGAAGAAGCA 1271
DB 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGlyLysGluPro 418
QY 1272 TTGGTTAGAGTTTGGTTAAACGACAGAGTGTTCATTGCACGGTGTGGTCTTCAAG 1331
DB 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1332 TTGGGTAGATGTAAGAGACGACTTCTGTTGAAGTTTGTCTTCCCTAGATCTGGTGT 1391
DB 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
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QY 1392 AACTGGGAAGNATGTTTCGCT 1412
DB 459 AsnTrpGlyGluCysPheSer 465

RESULT 9
US-09-636-499-6
: Sequence 6, Application US/09636499
: Patent No. 6475762
: GENERAL INFORMATION:
: APPLICANT: Stafford, Christian F.
: APPLICANT: Trinci, Anthony P.J.
: APPLICANT: Brookman, Jayne L.
: TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
: TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Sa
: FILE REFERENCE: GC586-2
: CURRENT APPLICATION NUMBER: US/09/636,499
: PRIOR FILING DATE: 2000-08-11
: PRIOR APPLICATION NUMBER: US 60/148,960
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 465
: TYPE: PR1
: ORGANISM: Aspergillus fumigatus
US-09-636-499-6

Alignment Scores:
Pred. No.: 6,6e-173 Length: 465
Score: 1902.00 Matches: 360
Percent Similarity: 85.01% Conservative: 37
Best Local Similarity: 77.09% Mismatches: 68
Query Match: 75.33% Indels: 2
Dh: 4 Gaps: 2

US-09-488-265B-25 (1-1426) x US-09-636-499-6 (1-465)

QY 12 ATGGCGGTGTTGTCGTGCTACTGTCATTCAGCCACCTGTTGGTCCACATCCGCTACC 71
DB 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 72 GCCTTGGGTCTCTGCTGTAATCTCTACTCTTTGTGACACTGTTGACGGTGGTTACCAATGT 131
DB 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 132 TTCACAAATTTTCACACTTGTGGGTCAATAGTCTCCATCTCTCTTGGCTGACGA 191
DB 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59
QY 192 TCTGCTATTCTCCAGACGTTCCAAAGGGTGTAGAGTTACTTTCGTTCAAGTTTGTCT 251
DB 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACACGGTCTAGATACCCACTTCTTCTAAGTCTAAGAAGTACTGCTTGTGATTGAA 311
DB 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysThrLysLysValThr 99
QY 312 GCTATTCAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTCTTGAAGACTTACAAC 371
DB 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 372 TACACTTGGGTGCTGACGACTTGAAGTCCATTGCTCGGTGAACAACAATGGTTAACTCTGT 431
DB 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 432 ATTAAGTTCTACAGAAGTACAGGCTTGGCTTGAAGAGATTGTTCCATTCTGTTAGACT 491
DB 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 492 TCTGGTCTGACAGAGTATTGCTTGTGCTGAAAGTTCATTGAAGGTTTCCAATCTGCT 551
DB 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179
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Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspLeuArg 238
QY 732 GCTAGATTGGAGCTCACTTCCAGGTTTAACCTTGACTGACGACAGAGCTTCTTACTTG 751
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 792 ATGGACATGCTGCCATTGCAACTGTTGCTAGAACTTCTGACGCTACTCAATGCTGCA 851
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 852 TTCTGTGACTTGTTCACGACGACGAATGGATTCAATACGACTACTTGCAATCTTGGGT 911
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysThrAsnTrpLeuGlnSerLeuGly 298
QY 912 AAGTACTACGTTACGTTGGTGTGTAACCCATTGGGTCACGCTCAAGGTTGGTTTCGT 971
Db 299 LysTrpTrpGlyTrpGlyAlaGlyAsnProLeuGlyProAlaGlnGlyLeuGlyPheThr 318
QY 972 AACGAATTGATTGTAGATTGACTCAGCTCCAGTTCAACACACACACTTCTACTAACCC 1031
Db 319 AsnGluLeuLeuAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1032 ACTTTGGACTTAACCCAGCTACTTCCCAATTGACGCTACTTTGTACGCTGACTTCTCT 1091
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTrpValAspPheSer 358
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QY 1152 TTGCTACTACTTCTGTTGAATCTATTGAAGAACTGACGCTTACGCTGCTTCTTGGACT 1211
Db 379 LeuSerArgThrSerValGluSerAlaLysLeuLeuAspGlyTrpSerAlaSerTrpVal 398
QY 1212 GTTCCATTGCTGCTAGACTTACGTTGAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
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QY 1392 AACTGGGAAGATGTTTCCCT 1412
Db 459 AsnTrpGlyGluCysPheSer 465
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RESULT 11

US-09-044-716-80

; Sequence 80, Application US/09044728

; Patent No. 6391605

; GENERAL INFORMATION:

; APPLICANT: KOSTREWA, Dirk

; APPLICANT: PASAMONTES, Luis

; APPLICANT: TOMSCHY, Andrea

; APPLICANT: van LOON, Adolphus

; APPLICANT: VOGEL, Kurt

; APPLICANT: WYSS, Markus

; TITLE OF INVENTION: MODIFIED PHYTASES

; FILE REFERENCE: Modified Phytases

; CURRENT APPLICATION NUMBER: US/09/044,718

; CURRENT FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: EP 97810175.6

; PRIOR FILING DATE: 1997-03-25

; NUMBER OF SEQ ID NOS: 82

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 80

; LENGTH: 465

; TYPE: PRT

; ORGANISM: Aspergillus fumigatus

US-09-044-716-80

Alignment Scores:

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276d. No.: 3,83e-172 Length: 465
Score: 1894.00 Matches: 359
Percent Similarity: 84.90% Conserved: 69
Best Local Similarity: 76.87% Mismatches: 67
Query Match: 75.01% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265B-25 (1-1426) x US-09-044-716-80 (1-465)

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QY 72 GCCTTGGGCTCTCGTGAATTTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTrpGlnCys 39
QY 132 TTCACGAATTTCTCACTTGTGGGGTCAATACTCTCCATTTCTTCTTCTTTGGCTGACAA 191
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTrpSerProPhePheSerLeuGluAspGlu 59
QY 192 TCTGCTATTCTCCAGACGCTTCCAAAGGGTTGTAGAGTTACTTTTCGTTCAAGTTTGCT 251
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACACGGTGTAGTACCACACTTCTTAACTTCTAAGAAGTACTGCTTCTTGTATTGAA 311
Db 80 ArgHisGlyAlaArgTrpThrSerSerLysSerLysTrpLysLysValThrValThr 99
QY 312 GCTATTCCAAAGAACGCTACTGCTTTCNAUGGTAAGTACGCTTCTTCTGGAAGACTTAC 371
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTrpAsn 119
QY 372 TACACTTTGGGTGCTGACGACTTTCACCTCCATTCCGTTCCGTTGAACACAAATGTTT 431
Db 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 432 ATTAAGTTCTACACAAATACAAAGGCTTTCGGCTAGAAAGATTGCTTCATTCGTAGAGCT 491
Db 140 IleLysPheTrpGlnArgTrpLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 492 TCTGTTTCTGACAGAGTTATTGCTTCTGCTGAAAGTTCATTGAAAGTTTCCAACTGCT 551
Db 160 SerGlySerAspArgValIleAlaSerGlyLysPheIleGlyPheGlnGlnAla 179
QY 552 AAGTTGGCTGACCCAGGCTTAACCCACACCAAGCTTCTCCACTTATTAACGTTATAT 611
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleLeu 198
QY 612 CCAGAAGGTGCTGTTTACACACACACTTTGGACACGCTTGTGTACTTCTTCTTCCCTT 671
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysTrpLysPheGluAla 218
QY 672 TCTGAATTTGGGTGACGAGCTTGAAGCTAAGTTCACCTGCTGCTTTCCTCTCCACTT 731
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 732 GCTAGATTGGAAGCTCACITGGCCAGGTTTAACTTGACTTGAC---GACCAACAGCTT 791
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 792 ATGGACATGCTCCATTCGACACTGTTGTAGAACTTCTGACGCTACTCAATGCTGCTCCA 851
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 852 TTCTGTGACTTGTTCACGACGAAATGGATTCAATACGACTACTTGCAATCTTGGGT 911
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTrpAsnTrpLeuGlnSerLeuGly 298
QY 912 AAGTACTACGTTTACGTTGGTGTGTTAACCCTTGGTCCAGCTCAAGGTTTGTGTTTCT 971
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: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: CURRENT FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 12
: LENGTH: 449
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Alignment Scores:
Pred. No.: 5,21e-172 Length: 449
Score: 1892.50 Matches: 352
Percent Similarity: 88.41% Conservative: 37
Best Local Similarity: 80.00% Mismatches: 50
Query Match: 74.95% Indels: 1
DB: 4 Gaps: 1

US-09-488-265b-25 (1-1426) x US-09-044-718-12 (1-449)
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QY 153 TGGGGTCAATCTCCATCTCTCTCTTGGGTGAGCAATCTGCTATTCTTCACGACGTT 212
DB 31 TrpGlyGlnTyrSerProPheSerLeuGluAspGluLeuSerValSerLysLeu 50
QY 213 CCAAGGGTGTAGAGTACTTCTGCTCAAGTTTCTGCTAGACAGGCTGCTAGACGCA 272
DB 51 ProLysAspCysA:GleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 70
QY 273 ACTTCTCTAGCTCAGACAGTACTCTGCTTTCGATGAGCAATCTCAAAAGACGCTACT 332
DB 71 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 90
QY 333 GCTTTCAGGGTAAAGTACGCTTCTTGAAGACTTACAACTACACTTTGGTCTGACGAC 392
DB 51 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 110
QY 393 TTGACTCATTCCGTTGACACAAATGTTAACTCTGGTATTAAAGTTCTACAGACATAC 452
DB 111 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 130
QY 453 AAGGCTTGGCTAGAAAGATTGTTCCATTCTGCTAGAGTCTTGGTCTGACAGATTAT 512
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QY 573 RACCCACACCAAGCTTCTCCAGTTATTAAAGTTATTATTCAGAGGCTGCTGTTACAC 632
DB 171 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 189
QY 633 AACACTTTGGACCAAGCTTTGTGCTACTGCTTTCCAAAGATCTCAATTTGGGTGACGACGTT 692
DB 190 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 209
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DB 230 ProGlyValThrLeuThrAspGluAspValValSerLeu:MetAspMetCysSerPheAsp 249
QY 813 ACTGTTGCTAGAACTTCTGACGCTACTCAATGTCTCCATCTCTGIGACTTGTCTCACTAC 872
DB 250 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 269
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QY 933 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCTTAAACGAATTTGATGCTAGATIG 992
DB 290 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 309
QY 993 ACTCACTCTCCAGTTTCAAGACACACTTCTACTACCCACACTTTGGACTCTTACCCAGCT 1052
DB 310 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 329
QY 1053 ACTTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCTCACGACACACTATGGTTTCT 1112
DB 330 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 349
QY 1113 ATTTCTTCGCTTTGGGTGTTGTACACGCTACTAGGCAATGCTACTACTTCTCTGTTGAA 1172
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QY 1233 TACGTTGAATGATCCAAATGTGAAGCTGAAAGCAACCATTTGGTTAGAGTTTGGTTTAA 1292
DB 390 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 409
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RESULT 15
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: Sequence 82: Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: CURRENT FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 81
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-09-044-718-81

Alignment Scores:

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Pred. No.: 9,22e-172 Length: 465
Score: 1890.00 Matches: 358
Percent Similarity: 84.80% Conservative: 38
Best Local Similarity: 76.66% Mismatches: 69
Query Match: 74.85% Indels: 2
DB: 4 Gaps: 2

US-09-488-265B-25 (1-1426) x US-09-044-718-81 (1-465)

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QY 132 TTCCGCAAAATTCCTACTTGTGGGTCAATCTCTCCATCTTCCTTCCTTGGCTGACGAA 191
DB 40 SerProAlaThrSerHisLeuTyrGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 192 TCTGCTATTTCTCCAGACGTTCCAAAGGTTAGAGTTACITTCGTTCAAGTTTGCT 251
DB 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 75
QY 252 AGACACGGTCTAGATACCAACITCTCTTAAGTCTAAGAAGTACTCTCCTTIGATTGAA 311
DB 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99
QY 312 GCTATTCAAAGAACGCTACTGCTTCAAGGGTAAAGTACGCTTCTTGAAGACTTACAA 371
DB 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 372 TACACTTTGGTCTAGACACTGACTCCATTCGTTGACACACAAATGTTAACTCTGCT 431
DB 120 TyrThrLeuGlyAlaAspLeuThrAlaPheGlyGluGlnGlnLeuValAsnSerGly 139
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DB 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
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DB 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
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QY 1332 TTGGTAGATGTAAGACAGACGACTTCGTTGAAGCTTGTCTTTCCTAGATCTGCTGCT 1391
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 08:05:37 ; Search time 71.7378 Seconds

(without alignments)
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Perfect score: 2525

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 587654 seqs, 15821298: residues

Total number of hits satisfying chosen parameters: 1173308

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1 2311 91.5 467 14 US-10-083-452-9
2 1902 75.3 465 14 US-10-083-452-8
3 1902 75.3 465 15 US-10-062-848-78
4 1902 75.3 465 15 US-10-229-358-6
5 1898.5 75.2 474 15 US-10-213-990-24
6 1894 75.0 465 15 US-10-062-848-80
7 1893 75.0 465 15 US-10-062-848-79
8 1892.5 75.0 439 15 US-10-062-848-3
9 1892.5 75.0 449 15 US-10-062-848-12
10 1890 74.9 465 15 US-10-062-848-81
11 1868 74.0 469 15 US-10-062-848-82
12 1862 73.7 467 15 US-10-079-703-32
13 1862 73.7 467 15 US-10-229-358-5
14 1855 73.5 467 9 US-09-929-060-3
15 1850 73.3 467 14 US-10-083-452-11
16 1843 73.0 462 15 US-10-229-358-12
17 1820 72.1 444 15 US-10-062-848-1
18 1813.5 71.8 463 14 US-10-083-452-10
19 1813 71.8 443 9 US-09-929-060-1
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21 1798.5 71.2 447 15 US-10-062-848-6
22 1756 69.5 466 14 US-10-083-452-12
23 1756 69.5 466 15 US-10-229-358-7
24 1752 69.4 450 15 US-10-062-848-15
25 1719 68.1 466 14 US-10-083-452-13
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27 1702 67.4 438 15 US-10-062-848-2
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29 1661 65.8 489 15 US-10-229-358-10
30 1637 64.8 410 15 US-10-229-358-11
31 1395 55.2 475 14 US-10-083-452-14
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37 917 36.3 284 15 US-10-229-358-19
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ALIGNMENTS

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; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25

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: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version: 4.0
: SEQ ID NO: 9
: LENGTH: 467
: TYPE: PR1
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Variation
US-10-083-452-9

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Pred. No.: 2e-178      Length: 467
Score: 2311.00      Matches: 435
Percent Similarity: 95.93%      Conservative: 13
Best Local Similarity: 93.15%      Mismatches: 19
Query Match: 91.52%      Indels: 0
DB: 14      Gaps: 0

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QY 132 TTCCCGAATTTCTCACTTTGGGGTCAATACTCTCCATTCCTCTTCTTGGCTGACGAA 191
DB 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
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DB 161 SerGlySerAspArgValIleAsnAlaGluLysPheIleGluGlyPheGlnSerAla 180
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DB 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
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DB 361 HisAspAsnSerMetLysSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380
QY 1152 TTGCTACTACTTCTTGAATCTATGAAGAACTGACGGTTACGGTTCGCTTCTTGGACT 1211
DB 381 LeuSerThrThrSerValGluSerIleGluThrAspGlyTyrSerAlaSerTrpIhr 400
QY 1212 GTTCCATTCGCTGCTAGAGCTTACGTTCAATGTGCAATGTGAAGCTGAAAGTGAAGCA 1271
DB 401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420
QY 1272 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCAITGTCACGGTTCGTTGTTGACAA 1331
DB 421 LeuValatqValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440
QY 1332 TTGGGTAGATGTAAAGACAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGACTTGGT 1391
DB 441 LeuGlyArgCysLysArgAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
QY 1392 AACTGGGAAGAATGTTTCGCT 1412
DB 461 AsnTrpAlaGluCysPheAla 467

RESID: 2
US-10-083-452-8
: Sequence 8. Application: US/10093452
: Publication No. US20020127218A1
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618.500-US
: CURRENT APPLICATION NUMBER: US/10/063,452
: CURRENT FILING DATE: 2002-02-26
: PRIOR APPLICATION NUMBER: US/09/273,871
: PRIOR FILING DATE: 1999-03-22
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: PRIOR FILING DATE: 1998-06-25
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 8
: LENGTH: 465
: TYPE: PR1
: ORGANISM: Aspergillus fumigatus
```



```
Db 1 MetValThrLeuThrPheLeuSerAlaAlaTyrLeuSerGlyArgVa-SerAla 20
    ||| ||||| ||| |||
QY 72 GCCTGGGCTCGTGGTAAATCTCACACTCTGTGACACTGTGTACGGGTGTACCAATGT 131
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 132 TTCACGAATAATTTCTCACTGTGGGGTCAATACTCTCCATTCTCTCTTTCGGCAGACAA 191
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 40 SerProAlaThrSerHisLeuTyrGlyGlnTyrSerProPhePheSerLeuGluAspGly 59
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 192 TCTGCATTTCTCCACACTTCCAAAGGGTGTACAGTTCCTTTCCTCAAGTTCTCTCT 251
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 LeuSerValSerLysLeuProLysAspCysArgIleThrLeuValGlnVa-LeuSer 79
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 252 AGACAGGGTCTAGATACCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLeuValThr 99
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 312 GCTATTCCAAAGAACCTTACCTTTCAGGGTAACTAGCGCTTCTTCAAGACTTCAAC 371
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 372 TACACTTTGGGTGCTGACGACTTACCTCCATTCCGTGAACACAAATGTTAACTCTGGT 431
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnLeuVa-As-SerGly 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 432 ATTAAGTCTACAGAGATACAGAGCTTTGGCTAGAAAGATGTTCCTATTGGTAGACT 491
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerVa-ValProPheIleArgAla 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 492 TCTGGTTCTCACAGAGTTATTGCTCTGCTGAAAGTTCATTGAAGGTTTCCAACTCTGCT 551
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 552 AAGTTGCTACCCAGAGTCTAACCCACACCAAGCTCTCCAGTTATTAACTATTATT 611
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 612 CCAGAGGTGCTGGTTACACACACACTTTGGACCCAGGTTTGTGCTACTGCTTCCAGAA 671
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 199 ProGlnSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGlyAla 218
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 672 TCTGAATGGTGACAGCTTGAAGCTAACTTCACTGCTGTCTTTCCTCCACCTATTAGA 731
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 219 SerGlnLeuGlyAspGluAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 732 GCTAGATTGGAAGTCACCTTCCAGGTTTAACTTGACTGACCAAGAGCTTGTAACTTG 791
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValVa-SerLeu 258
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 792 ATGCACATGTCCATTCGACACTGTGTGAGAACTCTCTGACGCTACTCAATGTCGCA 851
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 279
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 852 ITCTGTGACTTGTCTACTCACGAGTAATTCATTAACGACTTCTGCAATCTTCTGGT 911
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 279 PheCysGlnLeuPheThrHisAsnGluTyrLysTyrAsnTyrLeuGlnSerLeuGly 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 912 AAGTACTACAGTGTGCTGTACCCATTGGGTCCAGCTCAAGGTGTGTGTTTCTGT 971
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 972 AACGAATTGATGTAGATGACTCTACTCTCCAGTTCAGAGACACACTTCTACTAACCCAC 1031
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1032 ACTTTGACTCTTACCCAGCTACTTTCCCATTTGAACGGCTACTTTGTACGCTGACTCTCT 1091
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1092 CACCACACACTATGTGTTCTATTCTTCTCGCTTTCGGTTTGTACACCGCTACTAGCCA 1151
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1152 TTGTCTACTACTTCTGTTGAATCTTGAAGAAATGACGAGTACGGTCTTCTTGGACT 1211
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 379 LeuSerArgThrSerValGlnSerAlaLysGlnLeuAspGlyTyrSerAlaSerTrpVal 398
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1212 GTTCCATTCGGTGTAGAGCTTACGTTGCAAAATGATGCAATCTGAAGCTGAAGACCA 1271
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGlnLysGluPro 418
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1272 TTGGTTAGAGTTTTCGTTAACGACAGAGCTTCTTCATTTCACGCTTCTGCTGACAAG 1331
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1332 TTGGTAGAATGATGACAGAGAGCTTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGT 1391
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1392 AACTGGGAAGAATGTTTCGCT 1412
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 459 AsnTrpGlyGluCysPheSer 465
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESUL 4
US-10-229-358-6
: Sequence 6, Application US/10229358
: Publication No. US20030124700A1
: GENERAL INFORMATION:
: APPLICANT: Stafford, Christian F.
: APPLICANT: Brookman, Jayne L.
: TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
: FILE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating San
: FILE REFERENCE: GC586-2
: CURRENT APPLICATION NUMBER: US/10/229,358
: CURRENT FILING DATE: 2002-08-26
: PRIOR APPLICATION NUMBER: US 60/148,960
: PRIOR FILING DATE: 1999-08-13
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 465
: TYPE: PRF
: ORGANISM: Aspergillus fumigatus
US-10-229-358-6

Alignment Scores:
Pred. No.: 2,46e-145 Length: 465
Score: 1902.00 Matches: 360
Percent Similarity: 85.01% Conservative: 37
Best Local Similarity: 77.09% Mismatches: 68
Query Match: 75.33% Indels: 2
DB: 15 Gaps: 2

US-09-488-265b-25 (1-1426) x US-10-229-358-6 (1-465)
QY 12 ATGGGGGTGCTGCTGCTGCTACTGTCTACTGTCCACTTCCACCTTGTTCGTTCCACATCGGTACC 71
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MetValThrLeuThrPheLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 72 GCCTGGGTCTCGTGGTGAATCTCACTCTTGTGACACTGTGTGACGTTGGTGTACCAATGT 131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 132 TTCCCAAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTCTCTTTCGGCAGACAA 191
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 40 SerProAlaThrSerHisLeuTyrGlyGlnTyrSerProPhePheSerLeuGluAspGly 59
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 192 TCTGCATTTCTCCACACTTCCAAAGGGTGTACAGTTCCTTTCCTCAAGTTCTCTCT 251
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 252 AGACAGGTGCTAGATACCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```



```
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysLysLeuValThr 39
QY 312 GCTATTCAAAACAGCGTACTGCTTTCAGAGGTAAAGTACCGCTTCTTGAGAGCTTACAAC 371
Db 100 AlalleGlnAlaAsnAlaThrAspPheCysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 372 TACACTTTGGTGGTGCAGACTTCACCTCCATTCGGTGAACAACAATGGTTTACCTGGT 431
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGlnGlnLeuValAsnSerGly 139
QY 432 ATTAGTTCTACAGAGATACAAGGCTTTCGGTAGAAGAGTTCATTCGCTACAGCT 491
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 492 TCTGCTTCACAGAGTTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
Db 160 SerGlySerAspArgValIleAlaSerGlyGlyLysPheIleGluGlyPheGlnAla 179
QY 552 AAGTGGCTGACCCAGGTGCTAACCCACACAGCTTCACAGTTCACAGTTCATATAT 611
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 596
QY 612 CCAGAGCTGCTGCTTACAAACACACTTCGACACAGCTTTCGCTGCTGCTGCTGCTGCTGCT 671
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 672 TCTGAATTCGGTGACGAGCTGAAGCTTAACCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
Db 219 SerGlnLeuLysAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 732 GCTAGATTGGAAGTCACTTCCAGGTGTTAACTTGACAGCAGCAGTGTGTAACCTG 791
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 256
QY 792 ATGCACATGCTGCTGACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 275
QY 852 TTCGTGACTTGTCTCACTCAGCAGCAATGATTCATACAGCACTACTTGCAATCTTGGGT 911
Db 279 PheCysGlnLeuPheThrHisAsnGluThrLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 912 AAGTACTACGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 972 AACGAATTGATTGCTAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 336
QY 1032 ACTTTGGACTTACCCAGCTACTTCCCAITGACCGCTACTTGTACGCTGCTGCTGCTGCTGCTGCT 1091
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1092 CACGACACACTATGTTTCTATTTCTCTGCTTGGGTGTTGTACAACGCTACTTAAGCCA 1151
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY 1152 TTGCTACTACTTCTGTTGAATCTATTGAAGAAGCTGACGGTACGCTGCTGCTGCTGCTGCTGCT 1211
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTyrVal 398
QY 1212 GTTCCATTGCTGCTAGAGCTTACGTTGAATGATGCAATGCTGAAGCTGAAGGACCA 1271
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1272 TTGGTAGAGTTTGGTTAACGACAGAGTGTTCATTCGACGCTTGGTGTGTTGACAAG 1331
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1332 TTGGTAGATGTAAGACAGCACTTCGTTGAAGGTTTGTCTTTCGGTAGATCTGGTGGT 1391
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
```

```
QY 1392 AACTGGGAAGAAATGTTTCGCT 1412
Db 459 AsnTrpGlyGluCysPheSer 465
```

RESULT 5

```
US-10-213-990-24
: Sequence 24, Application US/10213990
: Publication No. US20030082595A1
: GENERAL INFORMATION:
: APPLICANT: Jiang, Bo
: APPLICANT: Bussey, Howard
: APPLICANT: Storms, Reg
: APPLICANT: Roemer, Terry
: TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
: FILE REFERENCE: 10182-019-999
: CURRENT APPLICATION NUMBER: US/10/213-990
: CURRENT FILING DATE: 2002-08-05
: NUMBER OF SEQ. ID NOS: 72
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 24
: LENGTH: 474
: TYPE: PRT
: ORGANISM: Aspergillus
US-10-213-990-24
```

```
Alignment Scores:
Prod. No.: 4.76e-145 Length: 474
Score: 1898.50 Matches: 357
Percent Similarity: 84.89% Conservative: 42
Best Local Similarity: 75.95% Mismatches: 64
Query Match: 75.19% Indels: 7
Gaps: 2
```

US-09-488-265b-25 (1-1426) x US-10-213-990-24 (1-474)

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QY 3 TATGAATTCATGGCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 62
Db 12 TyrLeuLeuSerGlyAlaValAlaValLeuLeuLysArgSerArgValSerAlaAlaPro 31
QY 63 TCCGCTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 122
Db 32 SerSer-----AlaGlySerLysSerLysSerCysAspThrValAspLeuGly 45
QY 123 TACCAATGTTTCCCAAGAAATTCCTCACTTGTGGGGTCAATACCTCTCCTCACTTCTCTCTG 182
Db 46 TyrGlnCysSerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeu 65
QY 183 GCTGACGAATCTGCTATTTCTCCAGACGTTCCAAAGGTTGTAGAGTTACTTTCGTTCAA 242
Db 66 GluAspGluLeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGln 85
QY 243 GTTGTGTACACACGCTGCTAGATACCAACTTCTTAAGTCTAAGAGTACTCTGCT 302
Db 86 ValLeuSerArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysLysLys 105
QY 303 TTGATTGAAGCTATTCAAAGACGCTACTGCTTTCAGGGTAAGTACGCTTCTTTCGAG 362
Db 186 LeuValThrAlalleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLys 125
QY 363 ACTTACACTACACTTGGGTGCTGACGACTTCACTTCCATTCGCTGCTGCTGCTGCTGCTGCTGCT 422
Db 126 ThrTyrAsnTyrThrLeuGlyAlaAspLeuThrProPheGlyGlnGlnLeuVal 145
QY 423 AACTCTGTTATTAAGTTCTACAGAAGATACAAGGCTTTCGCTTGAAGAGTTCGTTCCATTC 482
Db 146 AsnSerGlyIleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPhe 165
QY 483 GTTAGAGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
Db 156 IleArgAlaSerGlySerAspArgValIleAlaSerGlyLysPheIleGluGlyPhe 185
```

```
QY 543 CAATCTGCTAAGTGGCTGACCCAGGTGTAAACCCACACCAAGCTCTCCAGTTATTAC 602
Db 186 GlnAlaLysLeuAlaAspProGlyAlaThr ---AsnArgAlaAlaProAlaLysSer 204
QY 603 GTTATTATCCAGAGGIGCTGGTTTACAAACACACTTGGACACCGGTTTGTACTGCT 462
Db 205 ValIleIleProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLys 224
QY 563 TTCAGAAATCTGAAT:GGTGACGAGGTGGAAGCTAACTTACCTGCTGCTTTTCGCTCA 722
Db 225 PheGluAlaSerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaPro 244
QY 723 CCTATTAGACTAGATTGGAAGCTACCTGCCAGGTGTTAACTTGACTGACCAAGACGCT 782
Db 245 AspIleArgAlaArgAlaGluLysHisLeuProGlyVal:ThrLeuThrAspLysVal 264
QY 783 GTTAACCTGATGACAT:GTGTCATTCGACACTGTGTGAGAACTTTCGACCTACTCAA 842
Db 265 ValSerLeuMetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGln 284
QY 843 TTGCTCCATCTGCTGACTTCTTCACTCAGCAGGATGATTCATACGACTACTTGCAG 902
Db 285 LeuSerProPheCysGlnLeuPheThrH:AsnGluTrpLysLysThrAsnTrpLeuGln 304
QY 903 ICTTTGGGTAACTACGCTTACGGTGTGTGATACCCATTGGGTCCAGCTCAAGGTGT 962
Db 305 SerLeuGlyLysTrpTyrglyTyrglyAlaGlyAsnProLeuGlyProAlaGlnGlyIle 324
QY 963 GGTTCGTTAACCAATGTATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACTCT 1022
Db 325 GlyPheThrAsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSer 344
QY 1023 ACTAACCACTTTGCACTTAACCCAGCTACTTTCCTCCATTGAAGCGTACTTTGTACGCT 1082
Db 345 ThrAsnSerThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTrpVal 364
QY 1083 GACTCTCTCACCACACACATGTTCTTCTATTCTTCTCGCTTTGGGTTGTACACGGT 1142
Db 365 AspPheSerHisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTrpAsnGly 384
QY 1143 ACTAAGCATTTGCTACTACTTCTGTGATCTATTGTAAGAACTGACGGTTACGCTGT 1202
Db 385 ThrGluProLeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTrpSerAla 404
QY 1203 TCTTGGACTGTTCCATCGCTGCTAGAGTTAGTGTGAATGATGCAATGTGAAGCTGAA 1262
Db 405 SerTrpValValProPheGlyAlaArgAlaTrpPheGluThrMetGln:CysLysSerGlu 424
QY 1263 AAGGAACCATTTAGAGTTTGGTTAAGCAGAGTGTGTTCCATTCGACGGTGTGGT 1322
Db 425 LysGluProLeuValArgAlaLeuIleAsnAspArgValVal:ProLeuHisGlyCysAsp 444
QY 1323 GTTGCAAGTTGGGTACATGTAGAGAGACGACTTCTGTTGAAGGTTTGTCTTCCGTA 1382
Db 445 ValAspLysLeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArg 464
QY 1383 TCTGGTGGTAACGGGAAGAAATGTTTCGCT 1412
Db 465 SerGlyCysTrpGlyGluCysPheSer 474
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RESULT 6

```
US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTRENA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
```

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; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
; US-10-062-848-80

Alignment Scores:
Pred. No.: 1,09e-144 Length: 465
Score: 1894.00 Matches: 359
Percent Similarity: 84.80% Conservative: 37
Best Local Similarity: 76.87% Mismatches: 69
Query Match: 75.01% Indels: 2
Db: 15 Gaps: 2
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US-09-488-265B-25 (1-1426) x US-10-062-848-80 (1-465)

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QY 12 ATGGCGGTGTTGCTGCTGCTACTGTCATGTCACACCTGTCGTTCCACATCCGTAAC 71
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QY 72 GCCTTGGTCTCTGCTGCTGCTAACTCTCTACTCTTGTGACACTGTTGACGGTGTACCA 131
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTrpGlnCys 39
QY 132 TTCGCAAAATTTCTCACTTGTGGGTCAAATCTCTCCATCTCTCTCTGCTGCTCAGCA 191
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTrpSerProPhePheSerLeuGluAspGlu 59
QY 192 TCTGCTATTCTCCAGACGTTCCAAAGGTTGTAGAGTTACTTCTGTTCAAGTTTGTCT 251
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACAGGTCCTGATACCCACTTCTTCTAAGTCTAAGACTACTCTGCTTGTGTTGATA 311
Db 80 ArgHisGlyAlaArgTrpProThrSerSerLysSerLysLysLysLysLysLysLys 99
QY 312 GCTATTCAAAGAAGCACTACTGCTTCAAAGGTAAGTAGGCTTCTTCTGAAGACTTACA 371
Db 100 AlalleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTrpAs 119
QY 372 TACACTTGGTCTCAGCAGCTGACTTCATTCGTTGCTGACACAAATGTTAACTCTAGT 431
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGlyGlnGlnLeuValAsnSerGly 139
QY 432 ATTAAGTTCTACAGAATACAGAGCTTTGGCTAGACAAATGTTCCATTCCTTAGAGCT 491
Db 140 IleLysPheTrpGlnArgTrpLysAlaLeuAlaArgSerValValProPheIleArgAla 159
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Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
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Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaLysSerValIleIle 198
QY 612 CCAGAAGGCTGCTGTTTACAAACACACTTTGGACCAAGGTTTGTGTACTGCTGCTGCA 671
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 672 TCTGAATTTGGTGCACGCTGACCTTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 732 GCTAGATTGGAAGCTCACTTGCAGGTGTTAACTTGACTGCTGACGAAGACGTTGTTAA 791
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: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/1C/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.5
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 81
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Alignment Scores:
Pred. No.: 2,3e-144 Length: 465
Score: 1890.00 Matches: 358
Percent Similarity: 84.80% Conservative: 38
Best Local Similarity: 76.66% Mismatches: 69
Query Match: 74.85% Indels: 2
DB: 15 Gaps: 2

US-09-488-265B-25 (1-1426) x US-10-062-848-81 (1-465)

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Alignment Scores:	
Pred. No.:	2.3e-144
Score:	1890.00
Percent Similarity:	84.80%
Best Local Similarity:	76.66%
Query Match:	74.85%
DB:	15
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	Conservative: 38
	Mismatches: 69
	Indels: 2
	Gaps: 2
US-09-488-2658-35 (1-3426) x US-10-062-848-81 (1-465)	

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QY 1152 TTGCTACTACTTCGTTGAATCATCTATTGAGAACTACCGGTTACGCTGCTTCTTGGACT 1211
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QY 1212 GTTCATTGCGTGTAGAGCTTACGTTGAATGATGCAATGTGGAAGCTGAAAAGGAACCA 1271
Db 399 ValProPheGlyAlaArgAlaTy:PheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1272 TTGTTAGAGTTTGTTTAACGACAGAGATTGTTCATTGCACGGTGTGCTGTGACAAG 1331
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QY 1332 TTGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGCTTCGCTAGACTGCTGCT 1391
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY 1392 AACTGGGAAGATGTTTCGCT 1412
Db 459 AsnTrpGlyGluCysPheSer 465

RESULT 1:
CS-19-062-848-82
: Sequence 82, Application US/10062846
: Publication NO. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062.848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044, 718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 978.0175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn ver. 2.1

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: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn ver. 2.1

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Oy 84; TTGTCCTCCTTCTCTCCACATCACTCATCTCC

; APPLICATION NUMBER: 09/233,510

; APPLICATION NUMBER: 09/233,510


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Db 21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyTyrGlnCys 40
QY 132 TTCCACAGAAATTTCTCAGCTTGGGGTCAATACTCTCCATCTCTCTCTTGGCTGAGCAA 191
Db 41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnIys 60
QY 192 TCTGCTATTCTCCAGACGCTTCCAAAGGGTGTGTAGAGTACTTTCGTTCAAGTTTGTCT 251
Db 61 SerAlaIleSerProAspValProAlaGlyCysHisValThrPheAlaGlnValLeuSer 60
QY 252 AGACAGGGTGCTAGATACCCAACTCTCTTAAGTCTAAGAGTCTGCTTCATTGAA 311
Db 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleu 100
QY 312 GCTATTCAAGAAGCGCTACTGCTTTCAAGGGTAAGTACGGCTTTCTTGAAGACTTACAA 371
Db 101 GluIleGlnAsnAlaThrThrPheGluGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 372 TACACTTGGGTGCTGACGACTGACTCCTCATTCGGTGAACAACAAGTGTAACTCTGCT 431
Db 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 432 ATTAAGTCTACAGAGATACAAAGCTTTGGCTAGAAAGATTGTTCCTATCGTTAGAGCT 491
Db 141 ValLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 492 TCTGGTCTGACAGAGTATTGCTTCTGCTGCTGAAAGTTCATTGAAGTTTCCCATCTGCT 551
Db 161 SerGlySerSerArgValIleAlaSerGlyAsnLysPheIleGluGlyPheGlnSerThr 180
QY 552 AAGTGGCTGACCCAGGTGCTAACCCACCAAGCTCTCCAGTATTAACGTTATATT 611
Db 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle 200
QY 612 CCAGAAGTGGTGGTTACAAACACTTTGGACACGCTTTGGTGTACTGCTTTCGAAAGAA 671
Db 201 SerGluAlaSerThrSerAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 672 TCTGAATGGGTGACGACCTTCAAGCTCACTCTCACTGCTGTTCGCTCCACCTATTAGA 731
Db 221 SerGluLeuAlaAspPheIleGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 732 GCTAGATTGGAAGCTCATTGCCAGTGTTAACCTGACTGACGAGAGCGTTGTTAACTTG 791
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QY 972 AAGCAATTGATTGCTAGATTGACTCTCCACTCTCCACTTCAAGACCACTCTTCACTAACCA 1031
Db 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340
QY 1032 ACTTTCGACTCTAACCCACTACTTCCCATTTGACAGCTACTTTCACGCTGACTTCTCT 1091
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QY 1092 CACGCAACACTATGTTCTTCTTCTTCTGCTTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1151
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RESULT 15

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US-10-083-452-11
; Sequence 11. Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618,500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/99/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus ficum
US-10-083-452-11
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Pred. No.: 3,970-141 Length: 467
Score: 1850.00 Matches: 346
Percent Similarity: 83.51% Conservative: 44
Best Local Similarity: 74.09% Mismatches: 77
Query Match: 73.27% Indels: 0
DB: 14 Gaps: 0
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US-09-488-265b-25 (1-1426) x US-10-083-452-11 (1-467);

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QY 72 GCCTGGGTCCTCGTGGTAAATCTCCTACATCTTGTGACACIGTGTGACGGTGGTTACCAATGT 131
Db 21 AlaValProAlaSerArgAsnGlnSerThrValAspGlnGlyTyrGlnCys 40
QY 132 TTCCACAGAAATTTCTCAGCTTGGGGTCAATACTCTCCATCTCTCTCTTGGCTGAGCAA 191
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Db 41 PheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
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QY 252 AGACACGGTGTAGATACCCCAACTTCCTAAGTCTAAGAAGTACTCTGCTTCATTGAA 311
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Db 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIleGlu 100
QY 312 GCTATTCAAGAAGAGCTACTGCTTCAAGGGTAAAGTACGGTTCCTTGAAGACTTACAAC 371
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Db 101 GluIleGlnGlnAsnAlaThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 372 TACACTTTCGGTGTGACGAGCTTGACTCCATTCGCTGACCAACAAGTTCGTTAACTCTGGT 431
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Db 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTTGCCATTGCTTAGAGCT 491
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Db 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 492 TCTGTTCTGACAGAGATTATGCTTCTGCTGCAAAAGTTTCATGAAGGTTTCCATCTGCT 551
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Db 161 SerGlySerArgValIleAlaSerGlyLysPheIleGluGlyPheGlySerThr 180
QY 552 AAGTTGGTGTGACCCAGGCTGAACCCACCAAGCTCTCCAGTTATTAACTGTTATTAT 611
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Db 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle 200
QY 612 CCAGAAGTGTGGTGTATACAACACTTTGGACCAAGGTTTGTGTACTGCTTCCAAAGAA 671
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Db 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 672 TCTGATTGGGTGACGAGCTTGAAGCTTAACCTCACTGCTGTTTTCGCTCCACCTATTACA 731
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Db 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 732 GCTAGATTGGAGCTCACTTGCAGGTGTTAACCTGACTGACGAGAGCGTTTAACTTG 791
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Db 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
QY 792 ATGGACATGTGTCCATTGACACTGTTGCTAGAACTTCTGACGCTACTCAATGTCTCCA 851
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Db 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
QY 852 TTCTGTGCTTCTTCACTCAGCAGCAATGGATTCAATACGACTACTTGCACAACTTGGGT 911
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Db 381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaThrThr 400
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Db 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
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Db 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
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Job time : 95.7378 secs